```
                                GenCore version 4.5
                                Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run On:          June 18, 2002, 11:43:07 ; Search time 19.66 Seconds
                                             (without alignments)
                                             1055.712 Million cell updates/sec

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Scoring table:

Title:           US-09-454-651B-23
Perfect score:   1149
Sequence:        1 GLSHFCSGVIHVTKEVKEVA.........LRVNQTFNWNTTKQEHFPDN 216

Searched:        283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters:          283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Database :       PIR_71:*
                 1: pir1:*
                 2: pir2:*
                 3: pir3:*
                 4: pir4:*

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
```

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB ID	Description
1	1149	100.0	288	2	A45803	B-cell-restricted
2	1085	94.4	299	2	G00031	B7 protein - red-c
3	738	64.2	299	2	I46690	CD80 precursor - r
4	601.5	52.3	321	2	I54766	B-lymphocyte activ
5	561	48.8	309	2	I49503	B-lymphocyte activ
6	185	16.1	275	2	JC7604	CD86 spliced varia
7	182	15.8	329	1	A48754	CD86 antigen - hum
8	152	13.2	309	2	A48522	B7-2 antigen - hum
9	140.5	12.2	330	2	I46691	gene B7-2 protein
10	133.5	11.6	583	2	I46691	CD86 precursor - r
11	129	11.2	221	1	QQBE48	alcam - human
12	127	11.1	526	2	S70587	BARF1 protein - hu
13	122.5	10.7	588	2	JH0506	butyrophilin precu
14	122.5	10.7	588	2	A45254	adhesion molecule
15	120.5	10.5	509	2	JC5288	surface glycoprote
16	120.5	10.5	513	2	JC5289	SHP substrate-1 pr
17	118	10.3	487	2	S65133	butyrophilin - mou
18	116.5	10.1	1088	1	IJXLNL	neural cell adhesi
19	115	10.0	761	1	IJHUNG	neural cell adhesi
20	112.5	9.8	725	2	JE0099	neural cell adhesi
21	110.5	9.6	587	2	JH0464	DM-GRASP precursor
22	109.5	9.5	646	2	I38049	cell surface glyco
23	109.5	9.5	853	1	IJBONC	neural cell adhesi
24	109	9.5	526	2	A37821	butyrophilin - bov
25	109	9.5	2029	1	TDFFLK	protein-tyrosine-p
26	108	9.4	871	1	I48696	protein-tyrosine k
27	108	9.4	881	1	I48697	protein-tyrosine k
28	107.5	9.4	5175	2	T20992	hypothetical prote
29	107.5	9.4	5198	2	T43290	hemicentin precurs
30	106.5	9.3	333	2	A31923	amalgam protein pr
31	106.5	9.3	858	1	IJRTNC	neural cell adhesi
32	106	9.2	267	2	PL0064	T-cell receptor be
33	105.5	9.2	1091	1	IJCHNL	neural cell adhesi
34	104.5	9.1	210	2	A56169	Ig kappa chain V r
35	104	9.1	307	1	RWMSBC	T-cell receptor V r
36	104	9.1	725	2	JE0100	neural cell adhesi
37	103.5	9.0	1092	1	JN0635	neural cell adhesi
38	103.5	9.0	480	2	A56182	fibroblast growth
39	103.5	9.0	725	1	IJMSNG	neural cell adhesi
40	103.5	9.0	1115	1	IJMSNL	neural cell adhesi
41	103	9.0	423	2	T29549	hypothetical prote
42	103	9.0	1273	2	T42405	sax-3 protein - Ca
43	102.5	8.9	503	2	JC5287	SHP substrate-1 pr
44	102	8.9	1443	2	I50600	neogenin - chicken
45	101	8.8	1033	2	S19247	cell adhesion prot

ALIGNMENTS

```
RESULT     1

A45803
B-cell-restricted antigen B7 precursor - human
N;Alternate names: B-lymphocyte activation antigen B7
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 29-Sep-1999
C;Accession: I54495; A45803
R;Selvakumar, A.; Mohanraj, B.K.; Eddy, R.L.; Shows, T.B.; White, P.C.; Dupont, B.
A;Residues: 1-288 <RES>
Immunogenetics 36, 175-181, 1992
A;Cross-references: GB:M83077; NID:g179327; PIDN:AAA58390.1; PID:g179329
A;Title: Genomic organization and chromosomal location of the human gene encoding the
R;Freeman, G.J.; Freedman, A.S.; Segil, J.M.; Lee, G.; Whitman, J.F.; Nadler, L.M.
J. Immunol. 143, 2714-2722, 1989
A;Title: B7, a new member of the Ig superfamily with unique expression on activated a
A;Reference number: A45803; MUID:90010147
A;Molecule type: DNA
A;Residues: 1-288 <RES>
A;Cross-references: GDB:CD80; CD28LG1; CD28
A;Genetics:
A;Cross-references: GB:M27533; NID:g184680; PIDN:AAA36045.1; PID:g306916
A;Gene: GDB:CD80; CD28LG1; CD28
A;Cross-references: GDB:251792; OMIM:112203
A;Map position: 3q13.3-3q21
A;Introns: 34/1; 140/1; 234/1; 266/1
A;Superfamily: B-lymphocyte restricted antigen B7
A;Keywords: transmembrane protein
F;1-26/Domain: signal sequence #status predicted <SIG>
F;248-264/Domain: transmembrane #status predicted <TMM>
A;Accession: A45803
A;Molecule type: mRNA
A;Residues: 1-288 <FRE>


Query Match        100.0%;   Score 1149;  DB 2;  Length 288;
Best Local Similarity   100.0%;
Matches 216;   Conservative  0;   Mismatches 0;   Indels 0;   Gaps 0;

Qy        1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLFMMSGDMNIWPE 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLFMMSGDMNIWPE 86

Qy       61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVRADFPTPS 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       87 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 146

Qy      121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206

Qy      181 NMTINHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
            ||||||||||||||||||||||||||||||||||||
```

```
Db   207 NMTTNHSFMCLIKYGHLRVNQTFNWNTIKQEHFPDN 242
         |||||||||||||||||||||||||||||||||||||
```

RESULT 2
G00031
B7 protein - red-crowned mangabey (fragment)
C;Species: Cercocebus torquatus (red-crowned mangabey, white-collared mangabey)
A;Accession: G00031
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-289 <VIL>
A;Cross-references: EMBL:U19833; NID:g644783; PIDN:AAA86700.1; PID:g644784
C;Genetics:
A;Gene: B7
C;Superfamily: B-lymphocyte restricted antigen B7

Query Match   94.4%; Score 1085; DB 2; Length 289;
Best Local Similarity 95.3%; Pred. No. 3.1e-80;
Matches 205; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

```
Qy    2 LSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEY 61
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   28 LSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEY 87

Qy   62 KNRTIFDITNNLSIVILALRPSDEGTYECVLKYEKDAFKREHLAEVTLSVKADFPTPSI 121
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   88 KNRTIFDITNNLSIVILALRPSDEGTYECVLKYEKDAFKREHLAEVTLSVKADFPTPSI 147

Qy  122 SDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFN 181
        |:||||:||||||||||||||||||||||:||||||||||||||||||:|||||||||||
Db  148 TDFEIPPSNIRRICSTSGGFPEPHLSWLENGELNAIDTTVSQDPETELYTVSSKLDFN 207

Qy  182 MTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
        ||||||:|||||||||||||||||||||:||||||
Db  208 MTTNHSFVCLIKYGHLRVNQTFNWNTPKQEHFPDN 242
```

RESULT 3
I46690
CD80 precursor - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
A;Accession: I46690
R;Isono, T.; Seto, A.
Immunogenetics 42, 217-220, 1995
A;Title: Cloning and sequencing of the rabbit gene encoding T-cell costimulatory molecul...
C;Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 29-Sep-1999
A;Accession: I46690
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-299 <ISO>
A;Cross-references: GB:D49843; NID:g755096; PIDN:BAA08643.1; PID:g755097
C;Superfamily: B-lymphocyte restricted antigen B7

Query Match   64.28%; Score 738; DB 2; Length 299;
Best Local Similarity 63.98%; Pred. No. 3.3e-52;
Matches 133; Conservative 36; Mismatches 39; Indels 0; Gaps 0;

```
Qy    4 HFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEYKN 63
        ||.||||:||||:|||||||:|||||:.|.|.|.:||||||:.:||||||:||:|||||||
Db   29 HFSSGISQVTKSVKEMAALSCDYNISIDELARMRIYWQKDQOMVLSISGQVEVWPEYKN 88

Qy   64 RTIFDITNNLSIVILALRPSDEGTYECVLKYEKDAFKREHLAEVTLSVKADFPTPSISD 123
        ||:.||.||||:::||||:|:.|||:||.:.::||.|:.:.|:||:||::|||||:.||:
Db   89 RTFPDIINNLSLMILALRLSDKGTYTVCVVQKNENGSFRREHLTSVTLSIRADFPVPSITD 148
```

```
Qy  124 FEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFNMT 183
        :.:|.:.||||:|.||||||||:||:|:::.|||||:|:||:||:|||||:|.|:|||:|
Db  149 IGHPDENVKRIRCSASGGFPEPRLAWMEDGEELNAVNTTVDQDLDTELYSVSSELDFNVT 208

Qy  184 TNHSFMCLIKYGHLRVNQTFNWNTTKQE 211
        .||||:|||||||.||||||:|:|||:|:
Db  209 NNHSIVCLIKYGELSVSQOIFPWSKPKQE 236
```

RESULT 4
I54766
B-lymphocyte activation antigen 7-1 precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 19-May-2000
C;Accession: I54766
R;Judge, T.A.; Liu, M.; Christensen, P.J.; Fak, J.J.; Turka, L.A.
Int. Immunol. 7, 171-178, 1995
A;Title: Cloning the rat homolog of the CD28/CTLA-4-ligand B7-1: structural and funct...
A;Reference number: I54766; MUID:95252184
A;Accession: I54766
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-321 <RES>
A;Cross-references: EMBL:U05593; NID:g453381; PIDN:AAA80154.1; PID:g453382
C;Superfamily: B-lymphocyte restricted antigen B7

Query Match   52.3%; Score 601.5; DB 2; Length 321;
Best Local Similarity 54.4%; Pred. No. 3.7e-41;
Matches 112; Conservative 35; Mismatches 58; Indels 1; Gaps 1;

```
Qy    1 GLSHFCSGVI-HVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWP 59
        ||| :.||:  ||:|||:|||||||:|: :::|.|.|::||||||:|:||::|||:.|.|
Db   31 GLLQISSGIVGQOVSKSVRERALLSCDYKFCSEEQSIHRIVWQKHDKRMVLSVISGVPEVWP 90

Qy   60 EYKNRTIFDITNNLSIVILALRPSDEGTYECVLKYEKDAFKREHLAEVTLSVKADFPTP 119
        :|||||. ||.|||||:| ::|||:.||||:||:|:::||:|:.||:.||::|.|||||
Db   91 KYKNRTVYDIFANNYSFSLLGLILSDRGTYICVCVQRYEGGSYVVKHLTTVELSVRADFPTP 150

Qy  120 SISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 179
        .|::. :|.:.||||:|.::||||:|:||:|:|:.:||.|:||:|:||||:||||.|:.|
Db  151 NITEYGNPSADIKRITCFASGGFPKPRLSWLENGRELNGINTTISQDPESELYITSSQLD 210

Qy  180 FNMTTNHSFMCLIKYGHLRVNQTFNWNTTKQE 211
        ||.|.:|:||:|:|:||:.||::.:|.|
Db  211 FNATVDHFIDCFIEYGDAHVSQNFTW 236
```

RESULT 5
I49503
B-lymphocyte activation antigen 7 precursor - mouse
N;Alternate names: MB7-2
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 29-Sep-1999
C;Accession: I49503; S17291; I49521
R;Selvakumar, A.; White, P.C.; Dupont, B.
Immunogenetics 38, 292-295, 1993
A;Title: Genomic organization of the murine B-lymphocyte activation antigen B7.
A;Reference number: I49503; MUID:9330789
A;Accession: I49503
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-309 <RES>
A;Cross-references: GB:L25589; NID:g293299; PIDN:AAA372240.1; PID:g293301
A;Accession: S17291
A;Reference number: S17291; MUID:91341422
R;Freeman, G.J.; Gray, G.S.; Gimmi, C.D.; Lombard, D.B.; Zhou, L.J.; White, M.; Finge...
J. Exp. Med. 174, 625-631, 1991
A;Title: Structure, expression, and T cell costimulatory activity of the murine homol...
A;Accession: S17291
A;Molecule type: mRNA
A;Residues: 1-274, 'R', 279-309 <FRE>
A;Cross-references: EMBL:X60958; NID:g50111; PIDN:CAA43291.1; PID:g50112
```

```
R;Inobe, M.; Linsley, P.S.; Ledbetter, J.A.; Nagai, Y.; Tamakoshi, M.; Uede, T.
Biochem. Biophys. Res. Commun. 200, 443-449, 1994
A;Reference number: I49521
A;Title: Identification of an alternatively spliced form of the murine homologue of B7.
A;Status: translated from GB/EMBL/DDBJ
A;Accession: I49521
A;Molecule type: mRNA
A;Residues: 1-143,238-274,'R',279-309 <RE2>
A;Cross-references: GB:D16220; NID:g505118; PIDN:BAA03748.1; PID:g994769
A;Genetics:
C;Genetics: B7
A;Introns: 37/1; 143/1; 237/1; 275/1
C;Superfamily: B-lymphocyte restricted antigen B7
C;Keywords: alternative splicing
```

```
Qy    Query Match    48.8%; Score 561; DB 2; Length 309;
      Best Local Similarity 50.7%;
Matches 104; Conservative 41; Mismatches 58; Indels 2; Gaps 2;

Qy  12 VTKEVEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEYKNRIIFDITN 71
Db  42 LSKSVKDKVLLPCRYNSPHEDESEDRIYWQKHDKVVLSVIAGKLKVWPEYKNRILYDNT- 100

Qy  72 NLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSISDFEIPTSNI 131
Db 101 TYSIILGLVLSDRGTYSCVVQKKERGTYEVKHLALVKLSIKADFSTPNITESGGNPSADT 160

Qy 132 RRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFNMTTNHSFMCL 191
Db 161 KRITCFASGGFPKPRFSWLENGRELPGINTTISQDPESELYTISSQLDENTTRNHTIKCL 220

Qy 192 IKYGHLRVNQTFNWNTIKQEHFPDN 216
Db 221 IKYGDAHVSEDFTWEKPPEDP-PDS 244
```

```
RESULT   6
JC7604
CD86 spliced variant CD86 deltaTM isoform - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
R;Magistrelli, G.; Caron, G.; Gauchat, J.F.; Jeannin, P.; Bonnefoy, J.Y.; Delneste, Y.
Biochem. Biophys. Res. Commun. 280, 1211-1215, 2001
A;Title: Identification of an alternatively spliced variant of human CD86 mRNA.
A;Reference number: JC7604; MUID:21092744; PMID:11162656
A;Accession: JC7604
A;Molecule type: mRNA
A;Residues: 1-275 <MAG>
C;Comment: This CD86 variant expressed by activated human monocytes, is a costimulatory
A;Residues: 1-275 <MAG>
A;Accession: JC7604
A;Molecule type: mRNA
A;Genetics:
C;Genetics:
A;Gene: cd86deltaTM
C;Keywords: immune response
```

```
Qy    Query Match    16.1%; Score 185; DB 2; Length 275;
      Best Local Similarity 27.4%;
Matches 65; Conservative 42; Mismatches 78; Indels 52; Gaps 12;

Qy  18 EVATLSC---GHNVSVEELAQTRIYWQKEKKMVLTMM----SGDMNIWPEYKNRIIFDI 69
Db  28 ETADLPCQFANSQNQSLSELV--VFWQDQENLVLNEVYLGKEKFDSVHSKYMGRTSFD- 83

Qy  70 TNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSISDFEIPTS 129
Db  84 SDSWTLRLHNLQIKDKGLYQCIIHHKKPTGMIRIHQMNSELSVLANFSQPEI----VPIS 139

Qy 130 NIR-----RIICSTSGGFPEP-HLSWLENGEELNAINTTV-------SQDPETELYAVS 175
Db 140 NITENVYINLTCSSIHGYPEPKKMSVL---LRTKNSTIEYDGIMQKSQDNVTELYDVS 194

Qy 176 SKLDF--NMTTNHSFMCLIKYGHLRVNQ----TFNWNTIKQE-----HFPD 215
```

```
Db 195 ISLSVSFPDVTSNMTIFCILETDKTRLLSSPFSIGTNTMEREESEGQTKKRREKIHIPE 251
```

```
RESULT   7
A48754
B7-2 antigen - human
N;Alternate names: B70 glycoprotein; CD86 antigen; CTLA-4 counter-receptor
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A48754; S39055
R;Freeman, G.J.; Gribben, J.G.; Boussiotis, V.A.; Ng, J.W.; Restivo Jr., V.A.; Lombar
Science 262, 909-911, 1993
A;Title: Cloning of B7-2: a CTLA-4 counter-receptor that costimulates human T cell pr
A;Reference number: A48754; MUID:94053735
A;Accession: A48754
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-329 <FRE>
A;Cross-references: GB:L25259; NID:g416368; PIDN:AAA58389.1; PID:g416369
A;Note: it is uncertain whether Met-1 or Met-7 is the initiator
R;Azuma, M.; Ito, D.; Yagita, H.; Okumura, K.; Phillips, J.H.; Lanier, L.L.; Sonoza,
Nature 366, 76-79, 1993
A;Title: B70 antigen is a second ligand for CTLA-4 and CD28.
A;Reference number: S39055; MUID:94050123
A;Accession: S39055
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 7-329 <AZU>
A;Cross-references: GDB:CD86; CD28LG2
A;Map position: 3q13.3-3q21
A;Cross-references: GB:U04343; NID:g439838; PIDN:AAB03814.1; PID:g439839
A;Cross-references: GDB:433597; OMIM:601020
C;Genetics:
A;Gene: GDB:CD86; CD28LG2
A;Superfamily: B7-2 antigen
C;Keywords: glycoprotein
```

```
Qy    Query Match    15.8%; Score 182; DB 1; Length 329;
      Best Local Similarity 29.0%;
Matches 60; Conservative 38; Mismatches 71; Indels 38; Gaps 10;

Qy  18 EVATLSC---GHNVSVEELAQTRIYWQKEKKMVLTMM----SGDMNIWPEYKNRIIFDI 69
Db  34 ETADLPCQFANSQNQSLSELV--VFWQDQENLVLNEVYLGKEKFDSVHSKYMGRTSFD- 89

Qy  70 TNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSISDFEIPTS 129
Db  90 SDSWTLRLHNLQIKDKGLYQCIIHHKKPTGMIRIHQMNSELSVLANFSQPEI----VPIS 145

Qy 130 NIR-----RIICSTSGGFPEP-HLSWLENGEELNAINTTV-------SQDPETELYAVS 175
Db 146 NITENVYINLTCSSIHGYPEPKKMSVL---LRTKNSTIEYDGIMQKSQDNVTELYDVS 200

Qy 176 SKLDF--NMTTNHSFMCLIKYGHLRV 199
Db 201 ISLSVSFPDVTSNMTIFCILETDKTRL 227
```

```
RESULT   8
I49522
gene B7-2 protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
C;Accession: I49522
R;Freeman, G.J.; Borriello, F.; Hodes, R.J.; Reiser, H.; Gribben, J.G.; Ng, J.W.; Kim
J. Exp. Med. 178, 2185-2192, 1993
A;Title: Murine B7-2, an alternative CTLA4 counter-receptor that costimulates T cell
A;Reference number: I49522; MUID:9405585
A;Accession: I49522
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-309 <RES>
```

A;Cross-references: GB:L25606; NID:g432478; PIDN:AAA79770.1; PID:g432479
C;Genetics:
A;Gene: B7-2
A;Accession: I39428
C;Superfamily: B7-2 antigen

RESULT 9
I46691
CD86 precursor - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 23-Jul-1999
R;Isono, T.; Seto, A.
Immunogenetics 42, 217-220, 1995
A;Title: Cloning and sequencing of the rabbit gene encoding T-cell costimulatory molecul
A;Reference number: I46689; MUID:95369849
A;Accession: I46691
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-330 <ISO>
A;Cross-references: GB:D49842; NID:g755098; PIDN:BAA08642.1; PID:g755099
C;Superfamily: B7-2 antigen

Query Match   13.2%; Score 152; DB 2; Length 309;
Best Local Similarity   26.1%; Pred. No. 6.7e-05;
Matches   52; Conservative 43; Mismatches 78; Indels 26; Gaps 10;

```
Qy   20 ATLSC-----GHNVSVEELAQTRIYWQKEKKMVL------TMMSGDMNIWPEYKNRIFDI 69
            :|:|     ||| : :| |||:||:||| |||        : |  |:| :|| :|| |
Db   36 AYLPCPFTKAQNISLSELV---VFWQDQQKLVLYEHYLGTEKLDSVN--AKYLGRTSFD- 89

Qy   70 TNNLSIVILALRPSDEGTYECVVLKYEK-DAFKREHLAEVTLSVKADFPTPSISDFEIP 127
            ||| : || | | |:| :|| |::| :  |  :  | :||   | |   |:| |
Db   90 RNNWTLRLHNVQIKDMGSYDCFIQKKPPIGSILLQQTLTE--LSVIANFSEPEIKLAQNV 147

Qy  128 TSNIR-RIICSTSGGFPEPHLSW--LENGEELNAINTTVSQDPETELYAVSSKLDFNM- 182
            |:| : :|:| :: :|:|| |  ::| ||| | :| | |:|:   | :|:: | : :
Db  148 TGNSGINLTCISKQGHPKPKKMFFLFLIINSTNEYGDNMQISQDNVTELFSISNSLSFPD 207

Qy  183 -TTNHSFMCLIKYGHLRVN 200
          ::::: :|:| ::|: :
Db  208 GVWHMIVVCVLETESMKIS 226
```

RESULT 10
I39428
alcam - human
C;Species: Homo sapiens (man)
C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 21-Jul-2000
R;Bowen, M.A.; Patel., D.D.; Li, X.; Modrell, B.; Malacko, A.R.; Wang, W.C.; Marquardt, H
J. Exp. Med. 181, 2213-2220, 1995
A;Title: Cloning, mapping, and characterization of activated leukocyte-cell adhesion
A;Reference number: I39428; MUID:95279947
A;Accession: I39428
A;Molecule type: mRNA
A;Residues: 1-583 <RES>
A;Cross-references: GB:L38608; NID:g886257; PIDN:AAB59499.1; PID:g886258

Query Match   11.6%; Score 133.5; DB 2; Length 583;
Best Local Similarity   24.5%; Pred. No. 0.0046;
Matches   37; Conservative 35; Mismatches 54; Indels 25; Gaps 7;

```
Qy   59 PEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPT 118
          ||| :     | |:|:|:| :  |||:|:| | ::  :|  | :  :|
Db   84 PEYKDR--LNLSENYTLSISNARISDEKRFVCMLVT-EDNVFEAPTIVKV------FKQ 133

Qy  119 PSISDFE-----IPTSNIRRI-ICSTSGGFPEPHLSWLENGEELNAINTTV-----SQD 166
          || :    :|   :::| |  || :      |: | ||| |  :     |
Db  134 PSKPEIVSKALFLETEQLKRLGDCISEDSYPDGNITWYRNGKVLHPLEGAVVIIFKKEMD 193

Qy  167 PETELIYAVSSKLDFNMT----TNHSFMCLIKY 194
          | :::  : |:|:  |      ||:| |  :
Db  194 PVFQLYTMTSTLEYKTTKADIQMPFTCSVTY 224
```

RESULT 11
Q0BE48
BARF1 protein - human herpesvirus 4 (strain B95-8)
C;Species: human herpesvirus 4, Epstein-Barr virus
C;Date: 25-Feb-1985 #sequence_revision 25-Feb-1985 #text_change 16-Jul-1999
R;Bankier, A.T.; Deininger, P.L.; Farrell, P.J.; Barrell, B.G.
Mol. Biol. Med. 1, 21-45, 1983
A;Title: Sequence analysis of the 17,166 bp EcoRI fragment C of B95-8 Epstein-Barr vi
A;Reference number: A93065; MUID:85035713
A;Accession: B43045; A03792; S33058
A;Molecule type: DNA
A;Residues: 1-221 <BAN>
A;Cross-references: EMBL:V01555; NID:g59074; PIDN:CAA24809.1; PID:g1334917
R;Baer, R.; Bankier, A.T.; Biggin, M.D.; Deininger, P.L.; Farrell, P.J.; Gibson, T.J.
Nature 310, 207-211, 1984
A;Title: DNA sequence and expression of the B95-8 Epstein-Barr virus genome.
A;Reference number: A03794; MUID:84270667
A;Contents: annotation; protein coding region
C;Superfamily: human herpesvirus 4 BARF1 protein

Query Match   11.8%; Score 129; DB 1; Length 221;
Best Local Similarity   27.0%; Pred. No. 0.0031;
Matches   43; Conservative 25; Mismatches 47; Indels 44; Gaps 8;

```
Qy   18 EVATLSCGHNVSVEELAQTRIYWQK-----------------EKKMVLTMMSGDMNIWPE 60
          :|  | |  :|:    : :  ||                   |||::| ||| || |
Db   19 QAVTAFLGERVTLTS-----YWRRVSLGPEIEVSWFKLGPGEQVLIGRMHHDV-IFIE 71

Qy   61 YKNRTIFDI--TNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEV-----TLSV-- 112
          : ||  | |  ::|  : : |  ::|    |:: :| ||| :|| | ||      |||
Db   72 WPFRGFPDIHRSANTFFLVVTAANISHDGNYLCRMKLGETEVIKQEHLSVVKPLTLSVHS 131

Qy  113 -KADFPTPSISDEIPTSNIRRIICSTSGGFPEPHLSWL 150
          :|  ||    :   :::| : | ::     |: || |
Db  132 ERSQFP----DFSVLI-----VTCIVNAFPHPHVQWL 159
```

RESULT 12
S70587
butyrophilin precursor - human
C;Species: Homo sapiens (man)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jul-2000
R;Taylor, M.R.; Peterson, J.A.; Ceriani, R.L.; Couto, J.R.

Biochim. Biophys. Acta 1306, 1-4, 1996
A;Title: Cloning and sequence analysis of human butyrophilin reveals a potential recepto
A;Accession: S70587
A;Reference number: S70587; MUID:96201696
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-526 <TAY>
A;Cross-references: EMBL:U39576; NID:g1326082; PIDN:AAC50489.1; PID:g1326083

```
Query Match          11.1%;   Score 127; DB 2;   Length 526;
Best Local Similarity   27.5%;   Pred. No. 0.014;
Matches    52;   Conservative   33;   Mismatches   84;   Indels   20;   Gaps   10;

Qy  16 VKEVATLSC--GHNVSYEELAQTRIYWQKEKKMVLTMMSG---DMNIWPEYKNRTIF--- 67
          :::  ||| |  :  ||
Db  42 VGEDAELPCRLSPNASAEHL-ELRWFRKKVSPAVLVHRDGREQEAEQMPEYRGRATLVQD 100

Qy  68 -DITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPPTPSISDFEI 126
Db 101 GIAKGRVALRIRGVRVSDDGEYTCF---FREDGSYEEAL--VILKVAALGSDPHIS-MQV 154

Qy 127 PTSNIRRIICSTSGGFPEPHLSW-LENGEELNAINTIVSQDPETE-LYAVSSKLDFNMTT 184
Db 155 QENGEICLECISVGWPFEPQVQWRTSKGEKFP--STSESRNPDEEGLFTVAASVIIRDTS 212

Qy 185 NHSFMCLIK 193
Db 213 TKNVSCYIQ 221
```

RESULT 13
JH0506
adhesion molecule SC1 precursor - chicken
C;Species: Gallus gallus (chicken)
A;Accession: JH0506; PS0270
R;Tanaka, H.; Matsui, T.; Agata, A.; Tomura, M.; Kubota, I.; McFarland, K.C.; Kohr, B.;
Neuron 7, 535-545, 1991
A;Title: Molecular cloning and expression of a novel adhesion molecule, SC1.
A;Reference number: JH0506; MUID:92030150
A;Molecule type: mRNA
A;Residues: 1-588 <TAN>
A;Cross-references: GB:S63276; NID:g238000; PIDN:AAB20170.1; PID:g238001
A;Experimental source: embryo
A;Accession: PS0270
A;Molecule type: protein
A;Residues: 34-48 <TAN1>
C;Comment: This protein is uniquely and transiently expressed on spinal cord motoneurons
C;Keywords: glycoprotein; transmembrane protein
F;1-33/Domain: signal sequence #status predicted <SIG>
F;34-568/Product: adhesion molecule SC1 #status predicted <TRA>
F;500-523/Domain: transmembrane #status predicted <TRA>
F;101,173,199,271,312,366,462,485,504/Binding site: carbohydrate (Asn) (covalent) #statu

```
Query Match          10.7%;   Score 122.5; DB 2;   Length 588;
Best Local Similarity   25.7%;   Pred. No. 0.036;
Matches    39;   Conservative   32;   Mismatches   54;   Indels   27;   Gaps   8;

Qy  59 PEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPT 118
Db  90 PDYKDR--LSLSENYTLSIKNARISDEKRFVCMLVI-EDDVSEEPTVVKV---------- 139

Qy 119 PS-----ISDFEIPTSNIRRI-ICSTSGGFPEPHLSWLENG------EELNAINTIVSQ 165
Db 140 PSQPEILHQADF-LETEKLKMLGECVVRDSYPEGNVTWYKNGRVLQPVEEVVVINLRKVE 198

Qy 166 DPETELYAVSSKLDFNMT----TNHSFMCLIKY 194
Db 199 NRSTGLFTMTSSLQYMPTKEDANAKFTCIVTY 230
```

RESULT 14
A45254
surface glycoprotein BEN precursor - chicken
C;Species: Gallus gallus (chicken)
A;Accession: A45254
A;Reference number: A45254
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-588 <POU>
A;Cross-references: EMBL:X64301; NID:g63087; PIDN:CAA45579.1; PID:g63088
C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 21-Jul-2000
R;Pourquie, O.; Corbel, C.; Le Caer, J.P.; Rossier, J.; Le Douarin, N.M.
Proc. Natl. Acad. Sci. U.S.A. 89, 5261-5265, 1992
A;Title: BEN, a surface glycoprotein of the immunoglobulin superfamily, is expressed
A;Reference number: A45254; MUID:92302224
C;Keywords: glycoprotein

```
Query Match          10.7%;   Score 122.5; DB 2;   Length 588;
Best Local Similarity   25.7%;   Pred. No. 0.036;
Matches    39;   Conservative   32;   Mismatches   54;   Indels   27;   Gaps   8;

Qy  59 PEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPT 118
Db  90 PDYKDR--LSLSENYTLSIKNARISDEKRFVCMLVT-EDDVSEEPTVVKV---------- 139

Qy 119 PS-----ISDFEIPTSNIRRI-ICSTSGGFPEPHLSWLENG------EELNAINTIVSQ 165
Db 140 PSQPEILHQADF-LETEKLKMLGECVVRDSYPEGNVTWYKNGRVLQPVEEVVVINLRKVE 198

Qy 166 DPETELYAVSSKLDFNMT----TNHSFMCLIKY 194
Db 199 NRSTGLFTMTSSLQYMPTKEDANAKFTCIVTY 230
```

RESULT 15
JC5288
SHP substrate-1 protein, 509 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 16-Apr-1997 #sequence_revision 09-May-1997 #text_change 20-Jun-2000
C;Accession: JC5288
R;Yanao, T.; Matozaki, T.; Amano, K.; Matsuda, Y.; Takahashi, N.; Ochi, F.; Fujioka,
Biochem. Biophys. Res. Commun. 231, 61-67, 1997
A;Title: Mouse and human SHPS-1: Molecular cloning of cDNAs and chromosomal localizat
A;Reference number: JC5287; MUID:97223399
A;Contents: Brain
A;Accession: JC5288
A;Molecule type: mRNA
A;Residues: 1-509 <YAM>
A;Cross-references: DDBJ:D87967; NID:g1864012; PIDN:BAA13520.1; PID:g1864013
C;Cross-references: This protein is a glycosylated receptor-like protein and plays a role in c
acts as a docking protein and induce translocation of SHP-2 from the cytosol to the
C;Genetics:
A;Gene: shps-1
A;Map position: 2

```
Query Match          10.5%;   Score 120.5; DB 2;   Length 509;
Best Local Similarity   25.9%;   Pred. No. 0.044;
Matches    59;   Conservative   42;   Mismatches   88;   Indels   39;   Gaps   15;

Qy   3 SHFCSGV----IHVTKEVKEVA------------TLSCGHNVSYEELAQTRIYWQK----EKKMVL 48
Db  23 SCFCTGVTGKELKVTQPEKSVSVAAGDSTVLNC---TLTSLLPVGPIKWTKRGVGQSRLLI 79

Qy  49 TMMSGDMNIWPEYKNRTIFDIT--NNL--SIVILALRPSDEGTYECVVLKYEKDAFKREH 104
Db  80 YSFTGEH--FPRVTN--VSDATKRNNMDFSIRISNVTPEDAGTYYCV--KFQKGPSEPDT 133

Qy 105 L------AEVTLSVKADFPPS-ISDFEIPTSNIRRIICSTSGGFPEP--HLSWLENGEEL 156
Db 134 EIQSGGGTEVYVLAKPSPPEVSGPADRGIPDQKV-NFTCKSHGFSPRNITLKWFKDGQEL 192
```

```
Qy   157   NAINTIVSQDPETELYAVSS--KLDFNMTTNHSFMCLIKYGHLRVNQT   202
             : :|||: :| :|| : ||  : ||:::::
Db   193   HHLETTVNPSGKNVSYNISSTVRVVLNSMDVHS-KVICEVAHTTLDRS   239
```

Search completed: June 18, 2002, 11:43:56
Job time: 49 sec

OM protein - protein search, using sw model

GenCore version 4.5
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Run on: June 18, 2002, 11:43:57 ; Search time 11.96 Seconds
(without alignments)
699.283 Million cell updates/sec

Title: US-09-454-651B-23
Perfect score: 1149
Sequence: 1 GLSHFCSGVIHVTKEVKEVA.........LRVNQTFNWNTKQEHFPDN 216

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Total number of hits satisfying chosen parameters: 105224

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1149	100.0	288	1	P33681	homo sapien CD80_HUMAN
2	738	64.2	299	1	P42070	oryctolagus CD80_RABIT
3	561	48.8	306	1	Q00609	mus musculu CD80_MOUSE
4	182	15.8	329	1	P42081	homo sapien CD86_HUMAN
5	161	14.0	302	1	O75144	homo sapien ICOL_HUMAN
6	152	13.2	309	1	P42082	mus musculu CD86_MOUSE
7	150.5	13.1	322	1	O9jh8	mus musculu ICOL_MOUSE
8	140.5	12.2	330	1	P42071	oryctolagus CD86_RABIT
9	134.5	11.7	583	1	Q61490	mus musculu C166_MOUSE
10	133.5	11.6	583	1	Q13740	homo sapien C166_HUMAN
11	129	11.2	221	1	P03228	epstein-bar BRF1_EBV
12	127	11.1	526	1	Q13410	homo sapien BRF1_HUMAN
13	122.5	10.7	588	1	O62556	gallus gall C166_CHICK
14	119	10.4	524	1	P16170	mus musculu BUTY_MOUSE
15	116.5	10.1	1088	1	P13592	xenopus lae NCA1_XENLA
16	115	10.1	761	1	P13591	homo sapien NCA2_HUMAN
17	115	10.0	848	1	P11364	homo sapien NCA1_HUMAN
18	115	10.0	321	1	P43121	feline leuk TCB_FLV
19	110.5	9.6	646	1	P31836	homo sapien MU8_HUMAN
20	109.5	9.5	853	1	P18892	bos taurus NCA1_BOVIN
21	109	9.5	526	1	P16621	bos taurus BUTY_BOVIN
22	109	9.5	2029	1	P97792	drosophila LAR_DROME
23	108.5	9.4	365	1	P15364	drosophila BUTY_DROME
24	107.5	9.4	333	1	P13596	mus musculu CXAR_MOUSE
25	106.5	9.3	858	1	Q99795	drosophila AMAL_DROME
26	105	9.1	319	1	P13590	rattus norv NCA1_RAT
27	105	9.1	1091	1	P36335	homo sapien A33_HUMAN
28	104	9.1	1092	1	P13594	gallus gall NCA1_CHICK
29	103.5	9.0	725	1	P13595	xenopus lae NCA2_XENLA
30	103.5	9.0	1115	1	P57087	mus musculu NCA2_MOUSE
31	103	9.0	298	1	Q90610	homo sapien JAM2_HUMAN
32	102	8.9	1443	1		gallus gall NEO1_CHICK
33	101.5	8.8	403	1	Q62151	mus musculu RAGE_MOUSE
34	100	8.7	413	1	P31398	manduca sex HEMO_MANSE
35	99.5	8.7	1338	1	P17948	homo sapien VGR1_HUMAN
36	98.5	8.6	365	1	P78310	homo sapien CXAR_HUMAN
37	98	8.6	278	1	P04218	rattus norv OX2G_RAT
38	98	8.5	298	1	Q9xt56	bos taurus JAM1_BOVIN
39	98	8.5	1333	1	P35969	mus musculu VGR1_MOUSE
40	97	8.4	1336	1	P53767	rattus norv VGR1_RAT
41	96.5	8.4	739	1	P19320	homo sapien VCA1_HUMAN
42	96	8.4	1020	1	P12960	mus musculu CONT_MOUSE
43	95.5	8.4	811	1	P34083	drosophila FS22_DROME
44	95.5	8.3	873	1	P34082	drosophila FS21_DROME
45	95.5	8.3	1348	1	P52583	coturnix co VGR2_COTJA

ALIGNMENTS

RESULT 1
CD80_HUMAN STANDARD; PRT; 288 AA.
ID CD80_HUMAN
AC P33681;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE T lymphocyte activation antigen CD80 precursor (Activation B7-1
DE antigen) (CTLA-4 counter-receptor B7.1) (B7) (BB1).
GN CD80 OR CD28LG1 OR CD28LG OR LAB7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphoid;
RX MEDLINE=90010147; PubMed=2794510;
RA Freeman G.J., Freedman A.S., Segil J.M., Lee G., Whitman J.F.,
RA Nadler L.M.;
RT "B7, a new member of the Ig superfamily with unique expression on
RT activated and neoplastic B cells.";
RL J. Immunol. 143:2714-2722(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92307753; PubMed=1377173;
RA Selvakumar A., Mohanraj B.K., Eddy R.L., Shows T.B., White P.C.,
RA Dupont B.;
RT "Genomic organization and chromosomal location of the human gene
RT encoding the B-lymphocyte activation antigen B7.";
RL Immunogenetics 36:175-181(1992).
RN [3]
RP SEQUENCE OF 35-38.
RX MEDLINE=91341422; PubMed=1714935;
RA Freeman G.J., Gray G.S., Gimmi C.D., Lombard D.B., Zhou L.-J.,
RA White M., Fingeroth J.D., Gribben J.G., Nadler L.M.;
RT "Structure, expression, and T cell costimulatory activity of the
RT murine homologue of the human B lymphocyte activation antigen B7.";
RL J. Exp. Med. 174:625-631(1991).
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=95088403; PubMed=7527824;
RA Lanier L.L., O'Fallon S., Somoza C., Phillips J.H., Linsley P.S.,
RA Okumura K., Ito D., Azuma M.;
RT "CD80 (B7) and CD86 (B70) provide similar costimulatory signals for T
RT cell proliferation, cytokine production, and generation of CTL.";
RL J. Immunol. 154:97-105(1995).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF 35-234.
RX MEDLINE=20125021; PubMed=10651405;
RA Ikemizu S., Gilbert R.J., Fennelly J.A., Collins A.V., Harlos K.,
RA Jones E.Y., Stuart D.I., Davis S.J.;
RT "Structure and dimerization of a soluble form of B7-1.";
RL Immunity 12:51-60(2000).
CC -!- FUNCTION: INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T
CC LYMPHOCYTES ACTIVATION. T CELL PROLIFERATION AND CYTOKINE

```
CC                                                                 RECEPTOR.
CC  -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC  -!- TISSUE SPECIFICITY: EXPRESSED ON ACTIVATED B CELLS, MACROPHAGES
CC      AND DENDRITIC CELLS.
CC  -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC  -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC  -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC  -!- DATABASE: NAME=PROW; NOTE=CD guide CD80 entry;
CC      WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd80.htm".
```

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DR   EMBL; M27533; AAA36045.1; -.
DR   EMBL; M83077; AAA58390.1; -.
DR   EMBL; M83072; AAA58390.1; JOINED.
DR   EMBL; M83073; AAA58390.1; JOINED.
DR   EMBL; M83074; AAA58390.1; JOINED.
DR   PIR; A45803; A45803.
DR   PDB; 1DR9; 10-JAN-01.
DR   MIM; 112203; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003600; Ig_like.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00410; IG_like; 1.
KW   Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
KW   Receptor; 3D-structure.
FT   SIGNAL        1     34
FT   CHAIN        35    288       T LYMPHOCYTE ACTIVATION ANTIGEN CD80.
FT   DOMAIN       35    242       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    243    263       POTENTIAL.
FT   DOMAIN      264    288       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       43    123       IG-LIKE V-TYPE DOMAIN.
FT   DOMAIN      155    223       IG-LIKE C2-TYPE DOMAIN.
FT   DISULFID     50    116
FT   DISULFID    162    216
FT   CARBOHYD     53     53       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD     89     89       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD     98     98       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    186    186       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    207    207       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    211    211       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    226    226       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    232    232       N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE   288 AA;  33048 MW;  BA453EE345288B1F4 CRC64;
```

```
Query Match             100.0%;  Score 1149;  DB 1;  Length 288;
Best Local Similarity   100.0%;  Pred. No. 3.5e-89;
Matches  216;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86

Qy   61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKRRHILAEVTLSVKADFPTPS 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   87 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 146

Qy  121 ISDFEIPTSNIRRILCSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  147 ISDFEIPTSNIRRICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206

Qy  181 NMTTNHSFMCLIKYGHLRVNQTFNWNTIKQEHFPDN 216
         ||||||||||||||||||||||||||||||||||||
Db  207 NMTTNHSFMCLIKYGHLRVNQTFNWNTIKQEHFPDN 242
```

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RESULT 2

ID   CD80_RABIT     STANDARD;      PRT;   299 AA.
AC   P42070;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   T lymphocyte activation antigen CD80 precursor (Activation B7-1
DE   antigen).
GN   CD80.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=B/J X CHBB:HM;
RX   MEDLINE=95369849; PubMed=7642234;
RA   Isono T., Seto A.;
RT   "Cloning and sequencing of the rabbit gene encoding T-cell
RT   costimulatory molecules.";
RL   Immunogenetics 42:217-220(1995).
CC  -!- FUNCTION: INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T
CC      LYMPHOCYTES ACTIVATION. T CELL PROLIFERATION AND CYTOKINE
CC      PRODUCTION IS INDUCED BY THE BINDING OF CD28 OR CTLA-4 TO THIS
CC      RECEPTOR.
CC  -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC  -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC  -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC  -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
```

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DR   EMBL; D49843; BAA08643.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003600; Ig_like.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00410; IG_like; 1.
KW   Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
KW   Receptor.
FT   SIGNAL        1     32       POTENTIAL.
FT   CHAIN        33    299       T LYMPHOCYTE ACTIVATION ANTIGEN CD80.
FT   DOMAIN       33    243       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    244    264       POTENTIAL.
FT   DOMAIN      265    299       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       42    122       IG-LIKE V-TYPE DOMAIN.
FT   DOMAIN      154    222       IG-LIKE C2-TYPE DOMAIN.
FT   DISULFID     49    115       POTENTIAL.
FT   DISULFID    161    215       POTENTIAL.
FT   CARBOHYD     52     52       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD     88     88       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD     97     97       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    122    122       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    185    185       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    206    206       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    210    210       N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE   299 AA;  33513 MW;  6744223E5CC91DE0 CRC64;
```

```
Query Match              64.2%;  Score 738;  DB 1;  Length 299;
Best Local Similarity    63.9%;  Pred. No. 8.9e-55;
Matches  133;  Conservative   36;  Mismatches   39;  Indels    0;  Gaps    0;
```

Qy   4 HFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEYKN 63
         ||| ||||||| || :|||| :|| ||:|::|||| || || ||||||||||||||||
Db   29 HFSSGISQVTKSVKEMAALSCDYNISIDELARMRIYWQKDQOMVLSIISGQVEWPEYKN   88

Qy   64 RTIFDITNNLSIVILALRPSDEGTYECVLKYEKDAFKREHLAEVTLSVKADPTPTPSISD 123
         | || ||| ||||||||||||||||||||||||||||||||||||| :|| || :|||||
Db   89 RTFPDIINNLSMILALRLSDKGTYTCVVQKNENGSFRREHLTRSVTLSITRADPFVPSITD 148

Qy 124 FEIPTSNIRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFNMT 183
         | :|| ||||||||:||||||||||||||||||:||||||||||||||| :||:| :||
Db 149 IGHPDPNVKIRCSASGGFPEPRLAWMEDGEELNAVNTTVDQDLDTELYSVSSELDFNVT 208

Qy 184 TNHSFMCLIKYGHLRVNQTFNWNTTKQE 211
         ||:|| ||||||||||||||||||||||
Db 209 NNHSIVCLIKYGELSVSQIFPWSKPKQE 236

RESULT 3

CD80_MOUSE

ID CD80_MOUSE   STANDARD;   PRT;   306 AA.
AC Q00609;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE T lymphocyte activation antigen CD80 precursor (Activation B7-1
DE antigen) (B7).
GN CD80 OR B7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RX MEDLINE=91341422; PubMed=1714935;
RA Gray G.S., Freeman G.J., Gimmi C.D., Gribben J.G., Lombard D.B., Zhou L.J.,
RA White M., Fingeroth J.D., Gribben J.G., Nadler L.M.;
RT "Structure, expression, and T cell costimulatory activity of the
RT murine homologue of the human B lymphocyte activation antigen B7.";
RL J. Exp. Med. 174:625-631(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RX MEDLINE=93307789; PubMed=7686531;
RA Selvakumar A., White P.C., Dupont B.;
RT "Genomic organization of the mouse B-lymphocyte activation antigen
RT B7.";
RL Immunogenetics 38:292-295(1993).
CC -!- FUNCTION: INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T
CC   LYMPHOCYTES ACTIVATION. T CELL PROLIFERATION AND CYTOKINE
CC   PRODUCTION IS INDUCED BY THE BINDING OF CD28 OR CTLA-4 TO THIS
CC   RECEPTOR.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: EXPRESSED ON ACTIVATED B CELLS, GAMMA
CC   INTERFERON STIMULATED MONOCYTES AND NONCIRCULATING B-CELL
CC   MALIGNANCIES.
CC -!- DEVELOPMENTAL STAGE: EXPRESSED BETWEEN 4 AND 12 HOURS POST-
CC   ACTIVATION. PROTEIN WAS DETECTED AT CELL SURFACE AT 24 HOURS AND
CC   IT'S EXPRESSION WAS MAXIMAL FROM 48 TO 72 HOURS POST-ACTIVATION.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
DR EMBL; X60958; CAA43291.1; -.

DR EMBL; L12589; AAA37240.1; ALT_SEQ.
DR EMBL; L12585; AAA37240.1; JOINED.
DR EMBL; L12586; AAA37240.1; JOINED.
DR EMBL; L12587; AAA37240.1; JOINED.
DR EMBL; L12588; AAA37240.1; JOINED.
DR PIR; S17291; S17291.
DR MGD; MGI:1017775; Cd80.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 1.
DR SMART; SM00410; IG_like; 1.
KW Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
KW Receptor.
FT SIGNAL   1   37
FT CHAIN   38   306   T LYMPHOCYTE ACTIVATION ANTIGEN CD80.
FT DOMAIN   38   246   EXTRACELLULAR (POTENTIAL).
FT TRANSMEM   247   268   POTENTIAL.
FT DOMAIN   269   306   CYTOPLASMIC (POTENTIAL).
FT DOMAIN   47   126   IG-LIKE V-TYPE DOMAIN.
FT DOMAIN   158   246   IG-LIKE C2-TYPE DOMAIN.
FT DISULFID   54   119   POTENTIAL.
FT DISULFID   165   219   POTENTIAL.
FT CARBOHYD   93   93   N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD   99   99   N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD   149   149   N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD   189   189   N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD   210   210   N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD   214   214   N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE   306 AA; 34589 MW; 1DBADE0931B84C62 CRC64;

Query Match   48.8%; Score 561; DB 1; Length 306;
Best Local Similarity   50.7%; Pred. No. 5.9e-40;
Matches 104; Conservative 41; Mismatches 58; Indels 2; Gaps 2;

Qy   12 VTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEYKNRTIFDITN 71
          :||| || | |||||| ||:||||||||||||:|| |||| ||||||||||||:||| |
Db   42 LSKSVKDKVLLPCRYNSPHEDESEDRIYWQKHDKVVLSVIAGKLKVWPEYKNRTLYDNT- 100

Qy   72 NLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADPFPTPSISDFEIPTSNI 131
          ||| ||||||||||||||||| |||||||||||||||||||||| |||:||::
Db 101 TYSLIILGLVLSDRGTYSCVVQKKERGTYEVKHLALVKLSIKRADFSTPNIITESSGNPSADT 160

Qy 132 RRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFNMTTNHSFMCL 191
          || ||||||| ||||:|||| |:||||||| || |||||: |:|||||: |||:|| |
Db 161 KRITCFASGGFPKPRFSWLENGRELPGINTTISQDPESELYITSSQLDFNTIRNHTIKCL 220

Qy 192 IKYGHLRVNQTFNWNTTKQEHFPDN 216
          |||| |||||||||||||||: |:|
Db 221 IKYGDAHVSEDFTWEKPPEDP-PDS 244

RESULT 4

CD86_HUMAN

ID CD86_HUMAN   STANDARD;   PRT;   329 AA.
AC P42081; Q13655;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE T lymphocyte activation antigen CD86 precursor (Activation B7-2
DE antigen) (CTLA-4 counter-receptor B7.2) (B70) (FUN-1) (BU63).
GN CD86 OR CD28LG2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94057735; PubMed=7694363;
RA Freeman G.J., Gribben J.G., Boussiotis V.A., Ng J.W.,

RA   Restivo V.A. Jr., Lombard L.A., Gray G.S., Nadler L.M.;
RT   "Cloning of B7-2: a CTLA-4 counter-receptor that costimulates human T
RT   cell proliferation.";
RL   Science 262:909-911(1993).
RN   [2]
RP   SEQUENCE OF 7-329 FROM N.A.
RX   MEDLINE=94050123; PubMed=7694153;
RA   Azuma M., Ito D., Yagita K., Okumura K., Phillips J.H.,
RA   Lanier L.L., Somoza C.;
RT   "B70 antigen is a second ligand for CTLA-4 and CD28.";
RL   Nature 366:76-79(1993).
RN   [3]
RP   SEQUENCE OF 7-329 FROM N.A.
RC   TISSUE=Foreskin;
RX   MEDLINE=95331831; PubMed=7541777;
RA   Jellis C.L., Wang S.S., Rennert P., Borriello F., Sharpe A.H.,
RA   Green N.R., Gray G.S.;
RT   "Genomic organization of the gene coding for the costimulatory human
RT   B-lymphocyte antigen B7-2 (CD86).";
RL   Immunogenetics 42:85-89(1995).
RN   [4]
RP   CHARACTERIZATION.
RX   MEDLINE=95088403; PubMed=7527824;
RA   Lanier L.L., O'Fallon S., Somoza C., Phillips J.H., Linsley P.S.,
RA   Okumura K., Ito D., Azuma M.;
RT   "CD80 (B7) and CD86 (B70) provide similar costimulatory signals for T
RT   cell proliferation, cytokine production, and generation of CTL.";
RL   J. Immunol. 154:97-105(1995).
RN   [5]
RP   IDENTIFICATION AS CD86.
RX   MEDLINE=94348060; PubMed=7520767;
RA   Engel P., Gribben J.G., Freeman G.J., Zhou L.J., Nozawa Y., Abe M.,
RA   Nadler L.M., Wakasa H., Tedder T.F.;
RT   "The B7-2 (B70) costimulatory molecule expressed by monocytes and
RT   activated B lymphocytes is the CD86 differentiation antigen.";
RL   Blood 84:1402-1407(1994).
CC   -!- FUNCTION: RECEPTOR INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL
CC   FOR T LYMPHOCYTE PROLIFERATION AND INTERLEUKIN 2 PRODUCTION, BY
CC   BINDING CD28 OR CTLA-4. MAY PLAY A CRITICAL ROLE IN THE EARLY
CC   EVENTS OF T CELL ACTIVATION AND COSTIMULATION OF NAIVE T CELLS,
CC   SUCH AS DECIDING BETWEEN IMMUNITY AND ANERGY THAT IS MADE BY T
CC   CELLS WITHIN 24 HOURS AFTER ACTIVATION.
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- TISSUE SPECIFICITY: EXPRESSED BY ACTIVATED B LYMPHOCYTES AND
CC   MONOCYTES.
CC   -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC   -!- DATABASE: NAME=PROW; NOTE=CD guide CD86 entry;
CC   WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd86.htm".
CC   ---
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---
DR   EMBL; L25259; AAA58389.1; -.
DR   EMBL; U04343; AAB03814.1; -.
DR   EMBL; U17722; AAA86473.1; -.
DR   EMBL; U17717; AAA86473.1; JOINED.
DR   EMBL; U17718; AAA86473.1; JOINED.
DR   EMBL; U17719; AAA86473.1; JOINED.
DR   EMBL; U17721; AAA86473.1; JOINED.
DR   MIM; 601020; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS00290; IG_MHC; FALSE_NEG.
KW   Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
KW   Receptor.

```
FT   SIGNAL        1     23
FT   CHAIN        24    329       T LYMPHOCYTE ACTIVATION ANTIGEN CD86.
FT   DOMAIN       24    247       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    248    268       POTENTIAL.
FT   DOMAIN      269    329       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       33    117       IG-LIKE V-TYPE DOMAIN.
FT   DOMAIN      149    225       IG-LIKE C2-TYPE DOMAIN.
FT   DISULFID     40    110       POTENTIAL.
FT   DISULFID    157    218       POTENTIAL.
FT   CARBOHYD     33     33       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD     47     47       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    135    135       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    146    146       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    154    154       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    177    177       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    192    192       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    213    213       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CONFLICT     27     27       K -> E (IN REF. 3).
FT   CONFLICT     27     27       K -> E (IN REF. 3).
SQ   SEQUENCE   329 AA;  37696 MW;  65D4F3826889CF7D CRC64;
```

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Query Match             15.8%;  Score 182;  DB 1;  Length 329;
Best Local Similarity   29.0%;  Pred. No. 3.3e-08;
Matches   60;  Conservative   38;  Mismatches   71;  Indels   38;  Gaps   10;

Qy    18 EVATLSC----GHNVSVEELAQTRIVWQKEKKMVLFMM----SGDMNIWPEYKNRIFDI 69
            : :| : :   | ::| ::  ::  :| : :        ||
Db    34 ETADLPCQPANSQNQSLSELV---VFWQDQENLVLNEVYLGKEKFDSVHSKYMGRTSFD- 89

Qy    70 TNNLSIVILALRPSDEGTYECVVLKIYEKDAFKREHLAEVTLSVKADFPTPSISDFEIPTS 129
            : :  :  : : ||:|| |:| ::||    ||||
Db    90 SDSWTLRLHNLQIKDKGLYQCIIHHKKPTGMIRIHQMNSELSVLANFSQPEL----VPIS 145

Qy   130 NIR----RIICSTSGGFPEP-HLSWLENGEELNAINTTV----------SQDPETELYAVS 175
          ||:     :|||: ||:|||  : | :|| :    :            ||| ||||| |:|
Db   146 NITENVYINILCSSIHGYPEPKKMSVL-----LRTKNSTIEYDGIMQKSQDNVTELYDVS 200

Qy   176 SKLDF---NMTTNHSFMCLIKYGHLRV 199
           .|:    :: :|: |:|:|  | :|:|
Db   201 ISLSVSFPDVTSNMTIFCILETDKIRL 227
```

RESULT 5
ICOL_HUMAN
ID   ICOL_HUMAN   STANDARD;   PRT;   302 AA.
AC   O75144; Q9NR01; Q9HDI8;
DT   15-JUL-1999 (Rel. 38, Created)
DT   16-OCT-2001 (Rel. 41, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   ICOS ligand precursor (B7 homolog 2) (B7-H2) (B7-like protein G150)
DE   (B7-related protein-1) (B7RP-1).
GN   ICOSL OR B7H2 OR B7RP1 OR KIAA0653.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   TISSUE=Dendritic cell;
RX   MEDLINE=20477846; PubMed=11023515;
RA   Wang S., Zhu G., Chapoval A.I., Dong H., Tamada K., Ni J., Chen L.;
RT   "Costimulation of T cells by B7-H2, a B7-like molecule that binds
RT   ICOS.";
RL   Blood 96:2808-2813(2000).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.
RC   TISSUE=Peripheral blood lymphocytes;
RX   MEDLINE=20465019; PubMed=11007762;
RA   Yoshinaga S.K., Zhang M., Pistillo J., Horan T., Khare S.D., Miner K.,
RA   Sonnenberg M., Boone T., Brankow D., Dai T., Delaney J., Han H.,
RA   Hui A., Kohno T., Manoukian R., Whoriskey J.S., Coccia M.A.;
RT   "Characterization of a new human B7-related protein: B7RP-1 is the
RT   ligand to the co-stimulatory protein ICOS.";

```
RL   Int. Immunol. 12:1439-1447(2000).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM 2).
RC   TISSUE=Leukocyte;
RX   MEDLINE=20126021; PubMed=10657606;
RA   Ling V., Wu P.W., Finnerty H.F., Bean K.M., Spaulding V., Fouser L.A.,
RA   Leonard J.P., Hunter S.E., Zollner R., Thomas J.L., Miyashiro J.S.,
RA   Jacobs K.A., Collins M.;
RT   "Identification of GI50, a novel B7-like protein that functionally
RT   binds to ICOS receptor.";
RL   J. Immunol. 164:1653-1657(2000).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=98403880; PubMed=9734811;
RA   Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A.,
RA   Kotani H., Nomura N., Ohara O.;
RT   "Prediction of the coding sequences of unidentified human genes. X.
RT   The complete sequences of 100 new cDNA clones from brain which can
RT   code for large proteins in vitro.";
RL   DNA Res. 5:169-176(1998).
RN   [5]
RP   SEQUENCE FROM N.A. (ISOFORM 2).
RA   Ling V., Dunussi-Joannopoulos K.;
RT   "G150 molecules and uses therefor.";
RL   Patent number WO0121796, 29-MAR-2001.
CC   -!- FUNCTION: LIGAND FOR THE T-CELL-SPECIFIC CELL SURFACE RECEPTOR
CC       ICOS. ACTS AS A COSTIMULATORY SIGNAL FOR T-CELL PROLIFERATION AND
CC       CYTOKINE SECRETION; INDUCES ALSO B-CELL PROLIFERATION AND
CC       DIFFERENTIATION INTO PLASMA CELLS. COULD PLAY AN IMPORTANT ROLE IN
CC       MEDIATING LOCAL TISSUE RESPONSES TO INFLAMMATORY CONDITIONS, AS
CC       WELL AS IN MODULATING THE SECONDARY IMMUNE RESPONSE BY CO-
CC       STIMULATING MEMORY T-CELL FUNCTION (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC   -!- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; 1 (SHOWN HERE) AND 2;
CC       ARE PRODUCED BY ALTERNATIVE SPLICING.
CC   -!- TISSUE SPECIFICITY: ISOFORM 1 IS WIDELY EXPRESSED (BRAIN, HEART,
CC       KIDNEY, LIVER, LUNG, PANCREAS, PLACENTA, SKELETAL MUSCLE, BONE
CC       MARROW, COLON, OVARY, PROSTATE, TESTIS, LYMPH NODES, LEUKOCYTES,
CC       SPLEEN, THYMUS AND TONSIL), WHILE ISOFORM 2 IS DETECTED ONLY IN
CC       LYMPH NODES, LEUKOCYTES AND SPLEEN.
CC   -!- INDUCTION: CONSTITUTIVE EXPRESSION IS FURTHER ENHANCED BY
CC       TREATMENT WITH TNF-ALPHA IN PERIPHERAL BLOOD B-CELLS AND
CC       MONOCYTES, WHILE IT IS DECREASED IN DENDRITIC CELLS.
CC   -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. BTN/MOG
CC       SUBFAMILY.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC   -!- CAUTION: Ref.4 sequence differs from that shown in position 300
CC       onward for an unknown reason.
```

```
DR   EMBL; AF199028; AAF34739.1; -.
DR   EMBL; AF289028; AAG01176.1; -.
DR   EMBL; AF216749; AAK16241.1; -.
DR   EMBL; AB014553; BAA31628.1; ALT_SEQ.
DR   EMBL; AX100595; CAC36465.1; -.
DR   MIM; 605717; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003600; Ig_like.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00408; IG; 1.
DR   SMART; SM00410; IG_like; 1.
KW   Immune response; Glycoprotein; Transmembrane; Multigene family;
KW   Immunoglobulin domain; Signal; Glycoprotein;
KW   B-cell activation;
KW   Alternative splicing.
FT   SIGNAL         1     18       POTENTIAL.
FT   CHAIN         19    302       ICOS LIGAND.
FT   DOMAIN        19    256       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     257    277       POTENTIAL.
FT   DOMAIN       278    302       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN        30    120       IG-LIKE V-TYPE DOMAIN.
FT   DOMAIN       151    223       IG-LIKE C2-TYPE DOMAIN.
FT   DISULFID      37    113       POTENTIAL.
FT   DISULFID     158    216       POTENTIAL.
FT   CARBOHYD      70     70       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD     137    137       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD     173    173       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD     186    186       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD     225    225       N-LINKED (GLCNAC...) (POTENTIAL).
FT   VARSPLIC     300    302       GHV -> ESWNLLLLS (IN ISOFORM 2).
SQ   SEQUENCE   302 AA;  33349 MW;  647934E21B55E34A CRC64;
```

```
Query Match    14.0%;  Score 161;  DB 1;  Length 302;
Best Local Similarity   26.4%;  Pred. No. 1.7e-06;
Matches   57;  Conservative  36;  Mismatches  95;  Indels  28;  Gaps  8;

Qy   14  KEVKEV----ATLSCG-HNVSVEELAQTRIYWQ-KEKKMVLT----MMSGDMINWPEYKN  63
         :|: :|     :|:|   || |: |:  : :|| |.::|:|       :| ::| | :|
Db   23  KEVRAMVGSDVELSCACPEGSRFDLNDVVVYWQTSESKIVVTHIHIPQNSSLENVDSRYN  82

Qy   64  RTIFD----ITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKRADFPYP  119
         | : |     |::|  .:| |||:||||| || :|: ::  |:.||:|:||:| ||:: |
Db   83  RALMSPAGMLRGDFSLRLFNVTPQDEQKFHCLVLS-QSLGFQEVLSVEVTLHVAANFSVP  141

Qy  120  SISDFEIPTSNIRRIICSTSGGPPEPHLSWLENGEELNAINTTVSQDPETE------L  171
         : .   :|:|:   ||.|:|| |  :  | |:  |.  |: :.   :. |:      L
Db  142  VVSAPHSPSQDELTFTCTSINGYPRPNVYWINKTD----NSLLDQALONDTVFLNMRGL  196

Qy  172  YAVSSKLDFNMTTNHSFMCLIKYGHLRVNQTFNWNT  207
         | | ::| :.:  |:  || ||.  :::..: .  |
Db  197  YDVVSVLRIARTPSVNIGCCIENVLLQQNLTVGSQT  232
```

```
RESULT   6
ID   CD86_MOUSE                STANDARD;      PRT;   309 AA.
AC   P42082;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   T lymphocyte activation antigen CD86 precursor (Activation B7-2
DE   antigen) (Early T cell costimulatory molecule-1) (ETC-1).
GN   CD86.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94055585; PubMed=7504059;
RA   Freeman G.J., Borriello F., Hodes R.J., Reiser H., Gribben J.G.,
RA   Ng J.W., Kim J., Goldberg J.M., Hathcock K., Laszlo G., Lombard L.A.,
RA   Wang S., Gray G.S., Nadler L.M., Sharpe A.H.;
RT   "Murine B7-2, an alternative CTLA4 counter-receptor that costimulates
RT   T cell proliferation and interleukin 2 production.";
RL   J. Exp. Med. 178:2185-2192(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129;
RX   MEDLINE=96094437; PubMed=7499829;
RA   Borriello F., Oliveros J., Freeman G.J., Nadler L.M., Sharpe A.H.;
RT   "Differential expression of alternate mB7-2 transcripts.";
RL   J. Immunol. 155:5490-5497(1995).
RN   [3]
RP   SEQUENCE OF 7-309 FROM N.A.
RX   MEDLINE=94230971; PubMed=7513726;
```

RA "Chen C., Gault A., Shen L., Nabavi N.;
RT "Molecular cloning and expression of early T cell costimulatory
RT molecule-1 and its characterization as B7-2 molecule ";
RL J. Immunol. 152:4929-4936(1994).
-|- FUNCTION: RECEPTOR INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL
CC   FOR T LYMPHOCYTE PROLIFERATION AND INTERLEUKIN 2 PRODUCTION, BY
CC   BINDING CD28 OR CTLA-4. MAY PLAY A CRITICAL ROLE IN THE EARLY
CC   EVENTS OF T CELL ACTIVATION AND COSTIMULATION OF NAIVE T CELLS,
CC   SUCH AS DECIDING BETWEEN IMMUNITY AND ANERGY THAT IS MADE BY T
CC   CELLS WITHIN 24 HOURS AFTER ACTIVATION.
-|- SUBCELLULAR LOCATION: Type I membrane protein.
-|- TISSUE SPECIFICITY: EXPRESSED ON ACTIVATED B CELLS.
-|- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
-|- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
-|- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
-|- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-7 IS THE INITIATOR.

DR EMBL; L25606; AAA79770.1; -.
DR EMBL; U39456; AAC52334.1; -.
DR EMBL; U39459; AAC52334.1; -.
DR EMBL; U39461; AAC52334.1; JOINED.
DR EMBL; U39462; AAC52334.1; JOINED.
DR EMBL; U39461; AAC52334.1; JOINED.
DR EMBL; U39463; AAC52334.1; JOINED.
DR EMBL; U39464; AAC52334.1; JOINED.
DR EMBL; U39465; AAC52334.1; JOINED.
DR EMBL; U39466; AAC52334.1; JOINED.
DR EMBL; U39456; AAC52336.1; ALT_INIT.
DR EMBL; U39461; AAC52336.1; JOINED.
DR EMBL; U39462; AAC52336.1; JOINED.
DR EMBL; U39463; AAC52336.1; JOINED.
DR EMBL; U39464; AAC52336.1; JOINED.
DR EMBL; U39465; AAC52336.1; JOINED.
DR EMBL; U39466; AAC52336.1; JOINED.
DR EMBL; U39466; AAB30744.2; ALT_INIT.
DR EMBL; S70108; AAB30744.2; ALT_INIT.
DR MGD; MGI:101773; Cd86.
DR InterPro; IPR003006; .
DR InterPro; IPR003596; .
DR SMART; SM00406; IG_MHC; 1.
DR PROSITE; PS00290; IG_MHC; FALSE_NEG.
KW Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
KW Receptor.
FT SIGNAL   1   23   POTENTIAL.
FT CHAIN   24   309   T LYMPHOCYTE ACTIVATION ANTIGEN CD86.
FT DOMAIN   24   244   EXTRACELLULAR (POTENTIAL).
FT TRANSMEM   245   265   POTENTIAL.
FT DOMAIN   266   309   CYTOPLASMIC (POTENTIAL).
FT DOMAIN   33   117   IG-LIKE V-TYPE DOMAIN.
FT DOMAIN   149   223   IG-LIKE C2-TYPE DOMAIN.
FT DISULFID   40   110   POTENTIAL.
FT DISULFID   157   216   POTENTIAL.
FT CARBOHYD   33   33   N-LINKED (GLCNAC) (POTENTIAL).
FT CARBOHYD   47   47   N-LINKED (GLCNAC) (POTENTIAL).
FT CARBOHYD   92   92   N-LINKED (GLCNAC) (POTENTIAL).
FT CARBOHYD   135   135   N-LINKED (GLCNAC) (POTENTIAL).
FT CARBOHYD   146   146   N-LINKED (GLCNAC) (POTENTIAL).
FT CARBOHYD   154   154   N-LINKED (GLCNAC) (POTENTIAL).
FT CARBOHYD   175   175   N-LINKED (GLCNAC) (POTENTIAL).
FT CARBOHYD   190   190   N-LINKED (GLCNAC) (POTENTIAL).
FT CARBOHYD   231   231   N-LINKED (GLCNAC) (POTENTIAL).
SQ SEQUENCE   309 AA; 34665 MW; 8F58DCD1F881D5EA CRC64;

Query Match 13.2%; Score 152; DB 1; Length 309;
Best Local Similarity 26.1%;   Pred. No. 9.9e-06;
Matches 52; Conservative 43; Mismatches 78; Indels 26; Gaps 10;

Qy   20 ATLSC----GHNVSVEELAQTRIYWQKEKKMVL------TMMSGDMNIWPEYKNRTIFDI 69
            |.|| |||||...||..||| ::||.|| ||||
Db   36 AYLPCFFTKAQNISLSELV---VFWQDQQKLVLYEHYLGTEKLDSVN--AKYLGRTSFD- 89

Qy   70 TNNLSIVILALRPSDEGTYECVVLKYEK--DAFKREHLAEVTLSVKADFPTPSISDFEIP 127
            ||.|.. || ||||.|:..||:.. |.|.|:. .||:|::||..||.
Db   90 RNNWTLRLHNVQIKDMGSYDCFIQKKPPGSIILQQTLFE--LSVIANFSEPEIKLAQNV 147

Qy 128 TSNIR-RIICSTSGGFPEPHLSW--LENGEELNAINTTVSQDPEFELYAVSSKLDFNM-- 182
            ||:||.||||:||| ||| .|||..||||||...|||| ||::|:|||:|:||:||:
Db 148 TGNSGINLTCTSKQGHPKPKKMFLITNSTNEYGDNMQISQDNVTELFSISNSLSLSFPD 207

Qy 183 -TTNHSFMCLIKYGHLRVN 200
          .||||.|:|||.|.:|
Db 208 GVWHMTVVCVLETESMKIS 226

RESULT 7

ID ICOL_MOUSE   STANDARD;   PRT;   322 AA.
AC Q9QUJ8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE ICOS ligand precursor (B7 homolog 2) (B7-H2) (B7-like protein G150)
DE (B7-related protein-1) (B7RP-1) (LICOS).
GN ICOSL OR B7H2 OR B7RP1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.
RC TISSUE=Lymphocytes;
RX MEDLINE=20083495; PubMed=10617205;
RA Yoshinaga S.K., Whoriskey J.S., Khare S.D., Sarmiento U., Guo J.,
RA Horan T., Shih G., Zhang M., Coccia M.A., Kohno T., Tafuri-Bladt A.,
RA Brankow D., Campbell P., Chang D., Chiu L., Dai T., Duncan G.,
RA Elliott G.S., Hui A., McCabe S.M., Scully S., Shahinian A.,
RA Shaklee C.L., Van G., Mak T.W., Senaldi G.,
RA "T-cell co-stimulation through B7RP-1 and ICOS.";
RL Nature 402:827-832(1999).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Thymus;
RX MEDLINE=20015817; PubMed=10549624;
RA Swallow M.M., Wallin J.J., Sha W.C.;
RT "B7h, a novel costimulatory homolog of B7.1 and B7.2, is induced by
RT TNFalpha.";
RL Immunity 11:423-432(1999).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=C3H/HeJ; TISSUE=Fetal thymus;
RX MEDLINE=20126021; PubMed=10657606;
RA Ling V., Wu P.W., Finnerty H.F., Bean K.M., Spaulding V., Fouser L.A.,
RA Leonard J.P., Hunter S.E., Zollner R., Thomas J.L., Miyashiro J.S.,
RA Jacobs K.A., Collins M.;
RT "Identification of GL50, a novel B7-like protein that functionally
RT binds to ICOS receptor.";
RL J. Immunol. 164:1653-1657(2000).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Peripheral blood lymphocytes;
RX MEDLINE=21286479; PubMed=11390480;
RA Ling V., Wu P.W., Miyashiro J.S., Marusic S., Finnerty H.F.,
RA Collins M.;
RT "Differential expression of inducible costimulator-ligand splice
RT variants: lymphoid regulation of mouse g150-b and human g150
RT molecules.";
RL J. Immunol. 166:7300-7308(2001).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).

RA   Ling V., Dunussi-Joannopoulos K.;
RT   "G150 molecules and uses therefor.";
RL   Patent number WO0121796, 29-MAR-2001.
-!- FUNCTION: LIGAND FOR THE T-CELL-SPECIFIC CELL SURFACE RECEPTOR
    ICOS. ACTS AS A COSTIMULATORY SIGNAL FOR T-CELL PROLIFERATION AND
    CYTOKINE SECRETION; INDUCES ALSO B-CELL PROLIFERATION AND
    DIFFERENTIATION INTO PLASMA CELLS. COULD PLAY AN IMPORTANT ROLE IN
    MEDIATING LOCAL TISSUE RESPONSES TO INFLAMMATORY CONDITIONS, AS
    WELL AS IN MODULATING THE SECONDARY IMMUNE RESPONSE BY CO-
    STIMULATING MEMORY T CELL FUNCTION. DURING PREGNANCY, MAY FUNCTION
    TO SKEW THE CYTOKINE OF MATERNAL T-CELLS TOWARD IMMUNOPROTECTIVE
    TH2 PHENOTYPE.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; 1 (SHOWN HERE) AND 2/B;
    ARE PRODUCED BY ALTERNATIVE SPLICING.
-!- TISSUE SPECIFICITY: ISOFORM 1 HIGHEST EXPRESSION IN LYMPHOID
    TISSUES, SUCH AS SPLEEN (MOSTLY IN THE MARGINAL ZONE), LYMPH NODES
    (PARTICULARLY IN THE CORTEX AND IN BOTH PRIMARY AND SECONDARY
    FOLLICLES), THYMUS (PREDOMINANTLY IN THE MEDULLA), AND PEYER'S
    PATCHES (MOSTLY IN THE FOLLICLES), LOWER LEVELS IN MANY
    NONLYMPHOID TISSUES, SUCH AS BRAIN, HEART, KIDNEY, LIVER, LUNG,
    SKELETAL MUSCLE AND TESTIS. PRESENT ON FRESHLY ISOLATED SPLENIC B-
    CELLS, DENDRITIC CELLS AND MACROPHAGES. THE EXPRESSION OF
    ISOFORM 2 IS RESTRICTED TO HEART, SPLEEN AND KIDNEY.
-!- DEVELOPMENTAL STAGE: DETECTED EARLY IN HEMOPOIESIS; IN THE YOLK
    SAC AT 11.5 AND 12.5 DPC AND, TO A LESSER EXTENT, IN THE LIVER AT
    14.5 DPC.
-!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. BTN/MOG
    SUBFAMILY.
-!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
-!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.

DR   EMBL; AF216747; AAF45149.1; -.
DR   EMBL; AF199027; AAF34738.1; -.
DR   EMBL; AX100591; CAC36463.1; -.
DR   EMBL; AX100593; CAC36464.1; -.
DR   EMBL; AF394451; AAK77544.1; -.
DR   MGD; MGI:1354701; Icosl.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003600; Ig_like.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00410; IG_like; 1.
KW   B-cell activation; Immune response; Glycoprotein;
KW   Immunoglobulin domain; Signal; Transmembrane; Multigene family;
KW   Alternative splicing.
FT   SIGNAL   1   46   BY SIMILARITY.
FT   CHAIN   47   322   ICOS LIGAND.
FT   DOMAIN   47   277   EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   278   298   POTENTIAL.
FT   DOMAIN   299   322   CYTOPLASMIC (POTENTIAL).
FT   DOMAIN   55   145   IG-LIKE V-TYPE DOMAIN.
FT   DOMAIN   178   250   IG-LIKE C2-TYPE DOMAIN.
FT   DOMAIN   31   38   POLY-LEU.
FT   DOMAIN   289   292   POLY-ALA.
FT   DISULFID   62   138   POTENTIAL.
FT   DISULFID   185   243   POTENTIAL.
FT   CARBOHYD   71   71   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   120   120   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   163   163   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   200   200   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   213   213   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   252   252   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   265   265   N-LINKED (GLCNAC...) (POTENTIAL).
FT   VARSPLIC   321   322   HA -> TWAPVPYQDVLIPRVIMSPCLKTRGLP (IN
FT   ISOFORM 2).
FT   CONFLICT   237   237   R -> H (IN REF. 4 AND 5; CAC36464).
SQ   SEQUENCE   322 AA; 35960 MW; 55CCBA4AD12E47E6 CRC64;

Query Match   13.1%; Score 150.5; DB 1; Length 322;
  Best Local Similarity   27.1%; Pred. No. 1.4e-05;
  Matches   65; Conservative   32; Mismatches 102; Indels   41; Gaps   12;

Qy   2 LSHFC--SGVIHVTKEVKEVATLSCGHNVSVE-------ELAQTRIWQKEKKMV-----L 48
              |||| | :| ||| :|: |||| |
Db   38 LSSLCAASAETEVGAMVGSNVVLSC-----IDPHRHFNLSGLIYVWQIENPEVSVTYYL 92

Qy   49 TMMSGDMNIWPEYKNRTIFDITN----NLSIVILALRPSDEGTYECVVLKYEKDAFKREH 104
Db   93 PYKSPGINVDSSYKRGHLSLDSMKQGNFSLYLKNVTPQDTQEFTCRV--FMNTATELVK 150

Qy   105 LAE--VTLSVKADFPTP--SISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAIN 160
Db   151 ILEEVVRLRVAANFSTPVISTSDSSNPGQE-RTYICMSKNGYPENLYWI-NTTDNSLID 208

Qy   161 TTVSQDP----ETELYAVSSKLDFNMTTNHSFMCLIKYGHLRVN-------QTFWNNTTK 209
Db   209 TAIQNNTVYLNKLIGLIYDVISTLRLPWTSRGDVLCCVENVALHQNITSISQAESFIGNNTK 268

RESULT 8
CD86_RABIT
ID   CD86_RABIT   STANDARD;   PRT;   330 AA.
AC   P42071;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   B lymphocyte activation antigen CD86 precursor (Activation B7-2
DE   antigen).
GN   CD86.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=B/J X CHBB:HM;
RX   MEDLINE=95369849; PubMed=7642234;
RA   Isono T., Seto A.;
RT   "Cloning and sequencing of the rabbit gene encoding T-cell
RT   costimulatory molecules.";
RL   Immunogenetics 42:217-220(1995).
-!- FUNCTION: RECEPTOR INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL
    FOR T LYMPHOCYTE PROLIFERATION AND INTERLEUKIN 2 PRODUCTION, BY
    BINDING CD28 OR CTLA-4. MAY PLAY A CRITICAL ROLE IN THE EARLY
    EVENTS OF T CELL ACTIVATION AND COSTIMULATION OF NAIVE T CELLS,
    SUCH AS DECIDING BETWEEN IMMUNITY AND ANERGY THAT IS MADE BY T
    CELLS WITHIN 24 HOURS AFTER ACTIVATION.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
-!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
-!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.

DR   EMBL; D49842; BAA08642.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   SMART; SM00406; IGv; 1.
DR   SMART; SM00406; IG_MHC; 1.
DR   PROSITE; PS00290; IG_MHC; 1.

```
KW   Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
KW   Receptor.
FT   SIGNAL          1     22       POTENTIAL.
FT   CHAIN          23    330       B LIMPHOCYTE ACTIVATION ANTIGEN CD86.
FT   DOMAIN         23    247       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM      248    268       POTENTIAL.
FT   DOMAIN        269    330       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN         33    117       IG-LIKE V-TYPE DOMAIN.
FT   DOMAIN        149    225       IG-LIKE C2-TYPE DOMAIN.
FT   DISULFID       40    110       POTENTIAL.
FT   DISULFID      157    218       POTENTIAL.
FT   CARBOHYD       33     33       N-LINKED (GLCNAC...)  (POTENTIAL).
FT   CARBOHYD      135    135       N-LINKED (GLCNAC...)  (POTENTIAL).
FT   CARBOHYD      146    146       N-LINKED (GLCNAC...)  (POTENTIAL).
FT   CARBOHYD      154    154       N-LINKED (GLCNAC...)  (POTENTIAL).
FT   CARBOHYD      177    177       N-LINKED (GLCNAC...)  (POTENTIAL).
FT   CARBOHYD      192    192       N-LINKED (GLCNAC...)  (POTENTIAL).
FT   CARBOHYD      198    198       N-LINKED (GLCNAC...)  (POTENTIAL).
FT   CARBOHYD      213    213       N-LINKED (GLCNAC...)  (POTENTIAL).
SQ   SEQUENCE    330 AA;  37142 MW;  935CDD65C57E3EE1 CRC64;

Query Match             12.2%;  Score 140.5;  DB 1;  Length 330;
Best Local Similarity   27.4%;  Pred. No. 9.8e-05;
Matches  60;  Conservative  34;  Mismatches  84;  Indels  41;  Gaps  12;

Qy    18  EVATLSCGH-NVSVEELAQTRIYWQKEKKMVLTMM-----SGDMNIWPEYKNRIFDITN-  71
              | || || |||   ||||| ||   ::::||        : :  |  || :  :
Db    34  KTADLPCQFTNSQSRSLSELVVFWQDQERLVLYELFLGREKPDNVDPKYIGRTSFDQESW  93

Qy    72  NLSIVILALRPSDEGTYECVLKYEKDAFKREHLAEVTLSVKADFPTSISDFEIPTSNI  131
              |:|  |:|    |::||||  :  |   |      | | :::|  | ::
Db    94  NLQLHNVQIK--DKGVQCFVHRGARGLVPIIQMNSELSVLANFTQPEITT----LISNI  147

Qy   132  RR-----IICSTSGGFPEPHLSWLENGEELNAINTTV-------SQDPETELY-AVSS  176
              ::                                        |  ||| |
Db   148  TRNSAINLTCSSVQGYPEPKKMFF-----VLKTENATTEYDGVLEKSQDNVTGLYNISISG  203

Qy   177  KLDF-NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFP  214
              | |                   || |    |||
Db   204  SITFSDDIRNATIYCVL-------QTESTEIYSQ-HFP  233
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RL   J. Neurobiol. 25:831-845(1994).
-!- FUNCTION: CELL ADHESION MOLECULE THAT BINDS TO CD6. INVOLVED IN
CC       NEURITE EXTENSION BY NEURONS VIA HETEROPHILIC AND HOMOPHILIC
CC       INTERACTIONS. MAY PLAY A ROLE IN THE BINDING OF T AND B CELLS TO
CC       ACTIVATED LEUKOCYTES, AS WELL AS IN INTERACTIONS BETWEEN CELLS OF
CC       THE NERVOUS SYSTEM.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
-!- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
-!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE V-TYPE DOMAINS.
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DR   EMBL; U95030; AAC06342.1; -.
DR   EMBL; L25274; AAA37528.1; -.
DR   HSSP; Q13740; 1KJC.
DR   MGD; MGI:1313266; Alcam.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003600; Ig_like.
DR   Pfam; PF00047; ig; 5.
DR   SMART; SM00409; IG; 3.
DR   SMART; SM00410; IG_like; 2.
DR   PROSITE; PS00290; IG_MHC; FALSE_NEG.
DR   PROSITE; PS002290; IG_MHC; FALSE_NEG.
KW   Cell adhesion; Signal; Immunoglobulin domain; Glycoprotein; Transmembrane;
KW   Repeat; Signal.
FT   SIGNAL          1     27       POTENTIAL.
FT   CHAIN          28    583       CD166 ANTIGEN.
FT   DOMAIN         28    527       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM      528    549       POTENTIAL.
FT   DOMAIN        550    583       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN         28    263       IG-LIKE C2-TYPE DOMAIN 1.
FT   DOMAIN        263    321       IG-LIKE C2-TYPE DOMAIN 2.
FT   DOMAIN        347    399       IG-LIKE C2-TYPE DOMAIN.
FT   DOMAIN        428    492       IG-LIKE C2-TYPE DOMAIN 3.
FT   DISULFID       43    113       POTENTIAL.
FT   DISULFID      157    220       POTENTIAL.
FT   DISULFID      270    313       POTENTIAL.
FT   DISULFID      354    392       POTENTIAL.
FT   DISULFID      435    485       POTENTIAL.
FT   CARBOHYD       95     95       N-LINKED (GLCNAC...)  (POTENTIAL).
FT   CARBOHYD      167    167       N-LINKED (GLCNAC...)  (POTENTIAL).
FT   CARBOHYD      265    265       N-LINKED (GLCNAC...)  (POTENTIAL).
FT   CARBOHYD      306    306       N-LINKED (GLCNAC...)  (POTENTIAL).
FT   CARBOHYD      361    361       N-LINKED (GLCNAC...)  (POTENTIAL).
FT   CARBOHYD      457    457       N-LINKED (GLCNAC...)  (POTENTIAL).
FT   CARBOHYD      480    480       N-LINKED (GLCNAC...)  (POTENTIAL).
FT   CARBOHYD      499    499       N-LINKED (GLCNAC...)  (POTENTIAL).
FT   CONFLICT      227    227       PSGQKT -> AAGIPA (IN REF. 2).
FT   CONFLICT      232    232       S -> F (IN REF. 2).
FT   CONFLICT      454    454
SQ   SEQUENCE    583 AA;  65161 MW;  E7BAFA8FCA8F9489 CRC64;

Query Match             11.7%;  Score 134.5;  DB 1;  Length 583;
Best Local Similarity   25.2%;  Pred. No. 0.00063;
Matches  38;  Conservative  34;  Mismatches  54;  Indels  25;  Gaps  7;

Qy    59  PEYKNRIFDITNNLSIVILALRPSDEGTYECVLKYEKDAFKREHLAEVTLSVKADFPT  118
              || | |::  |  : |||||  | :|:  :   ||| :| |
Db    84  PEYKDR--LSLSENYTLSIANAKISDEKRFVCMLVT-EDNVFEAPTLYKV-----FKQ  133

Qy   119  PSISDFE-----IPTSNIRRI-ICSTSGGFPEPHLSWLENGEELNAINTTVS-----QD  166
              |:|    :  :|: :|::|    |:|||||
Db   134  PSKPEIVNKAPFLETDQLKKLGDCISRDSYPDGNITWRNGKVLQPVEGEVAILFKKEID  193

Qy   167  PETELYAVSSKLDFNMTTNH---SFMCLIKY  194
              |  ||  |||:    |     ||| |
Db   194  PGTQLYIVTSSLEYKTTRSDIQMPFTCSVTY  224
```

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RESULT 9
C166_MOUSE
ID   C166_MOUSE     STANDARD;     PRT;   583 AA.
AC   Q61490; O70136;
DT   01-NOV-1997 (Rel. 35, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   CD166 antigen precursor (Activated leukocyte-cell adhesion molecule)
DE   (ALCAM) (DM-GRASP protein).
GN   ALCAM.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NFS;
RX   MEDLINE=97753242; PubMed=9209500;
RA   Bowen M.A., Bajorath J., D'Egidio M., Whitney G.S., Palmer D.,
RA   Kobarg J., Starling G.C., Siadak A.W., Aruffo A.;
RT   "Characterization of mouse ALCAM (CD166): the CD6 binding domain is
RT   conserved in different homologs and mediates cross-species binding.";
RL   Eur. J. Immunol. 27:1469-1478(1997).
RN   [2]
RP   SEQUENCE OF 227-583 FROM N.A.
RC   STRAIN=BALB/C; TISSUE=Brain;
RX   MEDLINE=94376084; PubMed=8089660;
RA   Kanki J.P., Chang S., Kuwada J.Y.;
RT   "The molecular cloning and characterization of potential chick
RT   DM-GRASP homologs in zebrafish and mouse.";
```

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RESULT 10

ID   C166_HUMAN     STANDARD;      PRT;   583 AA.
AC   Q13740; O60892;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   CD166 antigen precursor (Activated leukocyte-cell adhesion molecule)
DE   (ALCAM).
GN   ALCAM OR MEMD.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95279947; PubMed=7760007;
RA   Bowen M.A., Patel D.D., Li X., Modrell B., Malacko A.R.,
RA   Wang W.-C., Marquardt H., Neubauer M., Pesando J.M., Francke U.,
RA   Haynes B.F., Aruffo A.;
RT   "Cloning, mapping, and characterization of activated leukocyte-cell
RT   adhesion molecule (ALCAM), a CD6 ligand.";
RL   J. Exp. Med. 181:2213-2220(1995).
RN   [2]
RX   MEDLINE=98161527; PubMed=9502422;
RA   Degen W.G., van Kempen L.C., Gijzen E.G., van Groningen J.J.,
RA   van Kooyk Y., Bloemers H.P., Swart G.W.;
RT   "MEMD, a new cell adhesion molecule in metastasizing human melanoma
RT   cell lines, is identical to ALCAM (activated leukocyte cell adhesion
RT   molecule).";
RL   Am. J. Pathol. 152:805-813(1998).
RN   [3]
RP   SEQUENCE OF 2-583 FROM N.A.
RX   MEDLINE=96420463; PubMed=8823162;
RA   Skonier J.E., Bowen M.A., Emswiler J., Aruffo A., Bajorath J.;
RT   "Recognition of diverse proteins by members of the immunoglobulin
RT   superfamily: delineation of the receptor binding site in the human
RT   CD6 ligand ALCAM.";
RL   Biochemistry 35:12287-12291(1996).
RN   [4]
RP   3D-STRUCTURE MODELING OF 28-133.
RX   MEDLINE=96060095; PubMed=8520490;
RA   Bajorath J., Bowen M.A., Aruffo A.;
RT   "Molecular model of the N-terminal receptor-binding domain of the
RT   human CD6 ligand ALCAM.";
RL   Protein Sci. 4:1644-1647(1995).
CC   -!- FUNCTION: CELL ADHESION MOLECULE THAT BINDS TO CD6. INVOLVED IN
CC       NEURITE EXTENSION BY NEURONS VIA HETEROPHILIC AND HOMOPHILIC
CC       INTERACTIONS. MAY PLAY A ROLE IN THE BINDING OF T AND B CELLS TO
CC       ACTIVATED LEUKOCYTES, AS WELL AS IN INTERACTIONS BETWEEN CELLS OF
CC       THE NERVOUS SYSTEM.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC   -!- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC   -!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE V-TYPE DOMAINS.
CC   -!- DATABASE: NAME=PROW; NOTE=CD guide CD166 entry;
CC       WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd166.htm".
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DR   EMBL; L38608; AAB59499.1; -.
DR   EMBL; Y10183; CAA71256.1; -.
DR   PDB; 1KJC; 03-APR-96.
DR   MIM; 601662; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003600; Ig_MHC; 2.
DR   Pfam; PF00047; ig; 5.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00410; IG_like; 5.
DR   PROSITE; PS00290; IG_MHC; FALSE_NEG.
DR   PROSITE; PS50290; IG_like.
KW   Cell adhesion; Immunoglobulin domain; Glycoprotein; Transmembrane;
KW   Repeat; Signal; 3D-structure; Polymorphism.
FT   SIGNAL        1     27       POTENTIAL.
FT   CHAIN        28    583       CD166 ANTIGEN.
FT   DOMAIN       28    527       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    528    549       POTENTIAL.
FT   DOMAIN      550    583       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       36    120       IG-LIKE V-TYPE DOMAIN 1.
FT   DOMAIN      150    227       IG-LIKE V-TYPE DOMAIN 2.
FT   DOMAIN      263    321       IG-LIKE C2-TYPE DOMAIN 1.
FT   DOMAIN      347    399       IG-LIKE C2-TYPE DOMAIN 2.
FT   DOMAIN      428    492       IG-LIKE C2-TYPE DOMAIN 3.
FT   DISULFID     43    113       POTENTIAL.
FT   DISULFID    157    220       POTENTIAL.
FT   DISULFID    270    313       POTENTIAL.
FT   DISULFID    354    392       POTENTIAL.
FT   DISULFID    435    485       POTENTIAL.
FT   CARBOHYD     91     91       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD     95     95       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    167    167       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    265    265       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    306    306       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    361    361       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    457    457       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    480    480       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    499    499       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    258    258       N-LINKED (GLCNAC...) (POTENTIAL).
FT   VARIANT     301    301       M -> S.
FT                                /FTId=VAR_003907.
FT   VARIANT     301    301       M -> T.
FT                                /FTId=VAR_003908.
SQ   SEQUENCE   583 AA;  65132 MW;  E023FB3974A60284 CRC64;

Query Match             11.6%;  Score 133.5;  DB 1;  Length 583;
Best Local Similarity   24.5%;  Pred. No. 0.00077;
Matches  37;  Conservative  35;  Mismatches  54;  Indels  25;  Gaps  7;

Qy    59 PEYKNRFIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAPRKEHLAEVTLSVKADPPT 118
            ||::|         :|:|||  |||  | |:|:|| ||:|  ||:|
Db    84 PEYKDR-LNLSENYTLSISNARISDEKRFVCMLVT-EDNVFEAPIIVKV-----FKQ 133

Qy   119 PSISDFE-----IPTSNIRRI-ICSTSGGFPEPHLSWLENGEELNAINTTTV-----SQD 166
            ::: |     |     ::| |:|::||:| |:|:|                 :: SQD
Db   134 PSKPEIVSKALFLETEQLKKLGSDCISEDSYPDGNITVWRNGKVLHPLEGAVVIIFKKEMD 193

Qy   167 PETELIAVSSKILDFNMT---TNHSFMCLIKY 194
            | ||| :: ::|| |      :: |:||: |
Db   194 PVTQLIYMTSTLEYKTIRKADIQMPFTCSVTY 224


RESULT 11

ID   BRF1_EBV       STANDARD;      PRT;   221 AA.
AC   P03228;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   33 kDa early protein (p33).
GN   BARF1.
OS   Epstein-barr virus (strain B95-8) (Human herpesvirus 4).
OC   Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC   Gammaherpesvirinae; Lymphocryptovirus.
OX   NCBI_TaxID=10377;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=84270667; PubMed=6087149;
```

RA   Baer R., Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J.,
RA   Gibson T.J., Hatfull G., Hudson G.S., Satchwell S.C., Seguin C.,
RA   Tuffnell P.S., Barrell B.G.;
RT   "DNA sequence and expression of the B95-8 Epstein-Barr virus genome.";
RL   Nature 310:207-211(1984).
RN   [2]
RP   IDENTIFICATION OF PROTEIN.
RX   MEDLINE=90059873; PubMed=2555151;
RA   Wei M.X., Ooka T.;
RT   "A transforming function of the BARF1 gene encoded by Epstein-Barr
RT   virus.";
RL   EMBO J. 8:2897-2903(1989).
CC   -!- FUNCTION: BARF1 HAS TRANSFORMING ACTIVITY.
CC   --
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --
DR   EMBL; V01555; CAA24809.1; -.
DR   PIR; A03792; QQBE48.
DR   PIR; S33058; S33058.
DR   InterPro; IPR003600; Ig_like.
SMART; SM00410; IG_like; 1.
KW   Early protein; Oncogene.
SQ   SEQUENCE   221 AA; 24471 MW; CA5A24D1EA28758E CRC64;

Query Match
Best Local Similarity 11.2%;
Matches 43; Conservative 25; Score 129; DB 1; Length 221;
Pred. No. 0.00055; Mismatches 47; Indels 44; Gaps 8;

Qy   18 EVATLSCGHNVSVEELAQTRIYWQK--------EKKMVLTMMSGDMNIWPE 60
         |:|: |||
Db   19 QAVTAFLGERVLTS------YWRRVSLGPEIEVSWFKLGPGEEQVLIGRMHHDV-IFIE 71

Qy   61 YKNRTIFDI---TNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEV---TLSV-- 112
         | ||| ||||||
Db   72 WPFRGFFDIHRSANTFFLVVTAANISHDGNYLCRMKLGETEVVRQEHLSVVKPLTLSVHS 131

Qy 113 -KADFPPTPSISDPEIPISNIRRIICSTSGGFPEPHLSWL 150
Db 132 ERSQFP-----DFSVLT------VTCTVNAFPHPHVQWL 159

RESULT 12
ID   BUTY_HUMAN   STANDARD;   PRT;   526 AA.
AC   Q13410;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Butyrophilin precursor (BT).
GN   BTN1A1 OR BTN.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Breast;
RX   MEDLINE=96201696; PubMed=8611614;
RA   Taylor M.R., Peterson J.A., Ceriani R.L., Couto J.R.;
RT   "Cloning and sequence analysis of human butyrophilin reveals a
RT   potential receptor function.";
RL   Biochim. Biophys. Acta 1306:1-4(1996).
CC   -!- FUNCTION: MAY FUNCTION IN THE SECRETION OF MILK-FAT DROPLETS. IT
CC   MAY ACT AS A SPECIFIC MEMBRANE-ASSOCIATED RECEPTOR FOR THE
CC   ASSOCIATION OF CYTOPLASMIC DROPLETS WITH THE APICAL PLASMA
CC   MEMBRANE (BY SIMILARITY).
CC   -!- SUBUNIT: SEEMS TO ASSOCIATE WITH XANTHINE DEHYDROGENASE/OXIDASE
CC   (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. BTN/MOG
CC   SUBFAMILY.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC   --
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --
DR   EMBL; U39576; AAC50489.1; -.
MIM; 601610; -.
DR   InterPro; IPR001870; Gamma_carbxylse.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   InterPro; IPR003877; SPRY.
DR   InterPro; IPR003878; SPRY_domain.
DR   Pfam; PF00047; Ig; 1.
DR   Pfam; PF00622; SPRY; 1.
SMART; SM00406; IGv; 1.
SMART; SM00449; SPRY; 1.
KW   Transmembrane; Glycoprotein; Immunoglobulin domain; Signal.
FT   SIGNAL   1   26   BY SIMILARITY.
FT   CHAIN   27   526   BUTYROPHILIN.
FT   DOMAIN   27   242   EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   243   269   POTENTIAL.
FT   DOMAIN   270   526   CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD   55   55   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   215   215   N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE   526 AA; 59004 MW; E9ECA0CF8DAF94D5 CRC64;

Query Match
Best Local Similarity 11.1%;
Matches 52; Conservative 33; Score 127; DB 1; Length 526;
Pred. No. 0.0024; Mismatches 84; Indels 20; Gaps 10;

Qy   16 VKEVATLSC--GHNVSVEELAQTRIYWQKEKKMVLTMMSG---DMNIWPEYKNRTIF--- 67
Db   42 VGEDAELPCRLSPNASAEHL-ELRWRFKKVSPAVLVHRDGREQEAPEQMPEYRGRATLVQD 100

Qy   68 -DITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPPTPSISDFEI 126
Db 101 GIAKGRVALRIRGVRVSDDGEYTCF---FREDGSYEEAL--VHLKVAALGSDPHIS-MQV 154

Qy 127 PTSNIRRIICSTSGGFPEPHLSW-LENGEELNAINTTVSQDPETE-LYAVSSKLDFNMTT 184
Db 155 QENGHICLECTSVGWYPEPQVQWRTSKGEKFP--STSESRNPDEGLFTVAASVIIRDTS 212

Qy 185 NHSFMCLIK 193
         |||: |
Db 213 TKNVSCYIQ 221

RESULT 13
ID   C166_CHICK   STANDARD;   PRT;   588 AA.
AC   P42292;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   CD166 antigen precursor (SC1 glycoprotein) (BEN glycoprotein) (DM-
DE   GRASP protein) (JC7 protein).
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]

```
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 34-53.
RC   TISSUE=Embryo;
RX   MEDLINE=92030150; PubMed=1931049;
RA   Tanaka H., Matsui T., Agata A., Tomura M., Kubota I.,
RA   McFarland K.C., Kohr B., Lee A., Phillips H.S., Shelton D.L.;
RT   "Molecular cloning and expression of a novel adhesion molecule, SC1.";
RL   Neuron 7:535-545(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91337449; PubMed=1873027;
RA   Burns F.R., von Kannen S., Guy L., Raper J.A., Kamholz J.,
RA   Chang S.;
RT   "DM-GRASP, a novel immunoglobulin superfamily axonal surface protein
RT   that supports neurite extension.";
RL   Neuron 7:209-220(1991).
RN   [3]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 34-52; 87-93; 504-512 AND 569-582.
RC   TISSUE=Bursa of fabricius;
RX   MEDLINE=92302224; PubMed=1608932;
RA   Pourquié O., Corbel C., le Caer J.-P., Rossier J., le Douarin N.M.;
RT   "BEN, a surface glycoprotein of the immunoglobulin superfamily, is
RT   expressed in a variety of developing systems.";
RL   Proc. Natl. Acad. Sci. U.S.A. 89:5261-5265(1992).
RN   [4]
RP   POSSIBLE FUNCTION.
RX   MEDLINE=92211411; PubMed=1311497;
RA   Pourquié O., Hallonet M.E.R., le Douarin N.M.;
RT   "Association of BEN glycoprotein expression with climbing fiber
RT   axonogenesis in the avian cerebellum.";
RL   J. Neurosci. 12:1548-1557(1992).
CC   -!- FUNCTION: HOMOPHILIC ADHESION MOLECULE ASSOCIATED WITH CLIMBING
CC       FIBER AXONOGENESIS. SUPPORTS NEURITE EXTENSION.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN A RESTRICTED POPULATION OF AXONS.
CC       WITHIN THE SPINAL CORD IT IS LOCALIZED TO AXONS IN THE DORSAL
CC       FUNICULUS, MIDLINE FLOOR PLATE CELLS, AND MOTONEURONS. FOUND IN
CC       DEVELOPING EPITHELIA, CENTRAL NERVOUS SYSTEM, AND HEMOPOIETIC CELLS. EACH
CC       DEVELOPING SYSTEM CARRIES DIFFERENTLY GLYCOSYLATED MOLECULAR FORMS
CC       OF BEN.
CC   -!- DEVELOPMENTAL STAGE: WIDELY EXPRESSED DURING EMBRYONIC
CC       DEVELOPMENT.
CC   -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC   -!- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC   -!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE V-TYPE DOMAINS.
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DR   EMBL; S63276; AAB20170.1; -.
DR   EMBL; M76678; AAA48602.1; -.
DR   EMBL; X64301; CAA45579.1; -.
DR   HSSP; Q13740; 1KJC.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003600; Ig_like.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00409; IG; 3.
DR   SMART; SM00410; IG_like; 2.
DR   PROSITE; PS00290; IG_MHC; FALSE_NEG.
KW   Cell adhesion; Immunoglobulin domain; Glycoprotein; Transmembrane;
KW   Repeat; Signal.
FT   SIGNAL        1     33
FT   CHAIN        34    588       CD166 ANTIGEN.
FT   DOMAIN       34    532       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    533    553       POTENTIAL.
FT   DOMAIN      554    588       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       42    126       IG-LIKE V-TYPE DOMAIN 1.
FT   DOMAIN      156    233       IG-LIKE V-TYPE DOMAIN 2.
FT   DOMAIN      269    326       IG-LIKE C2-TYPE DOMAIN 1.
FT   DOMAIN      352    404       IG-LIKE C2-TYPE DOMAIN 2.
FT   DOMAIN      433    497       IG-LIKE C2-TYPE DOMAIN 3.
FT   DISULFID     49    119       POTENTIAL.
FT   DISULFID    119    226       POTENTIAL.
FT   DISULFID    163    226       POTENTIAL.
FT   DISULFID    276    319       POTENTIAL.
FT   DISULFID    359    397       POTENTIAL.
FT   DISULFID    440    490       POTENTIAL.
FT   CARBOHYD    101    101       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    173    173       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    199    199       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    271    271       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    312    312       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    366    366       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    462    462       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    485    485       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    504    504       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CONFLICT      2      2       MEPPAAAAR -> EPPSRRRP (IN REF. 3).
FT   CONFLICT     25     25       A -> S (IN REF. 3).
FT   CONFLICT    112    113       SD -> RH (IN REF. 3).
FT   CONFLICT    329    329       A -> T (IN REF. 2).
FT   CONFLICT    401    402       LQ -> HK (IN REF. 2).
SQ   SEQUENCE   588 AA;  65726 MW;  2A28612D01645331E CRC64;
```

```
Qy   Query Match             10.7%;  Score 122.5;  DB 1;  Length 588;
     Best Local Similarity   25.7%;  Pred. No. 0.0064;
     Matches  39;  Conservative 32;  Mismatches 54;  Indels 27;  Gaps  8;

Qy        59 PEYKNRIFFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVILSVKADFPT 118
              || |:    |:|  :||| | |   ||||| |  |   :  |  ::   |  | |:
Db        90 PDYKDR--LSLSENYTLSIKNARISDEKRFVCMLVT-EDDVSEEPTVVKV------FKQ 139

Qy       119 PS-----ISDFEIPTSNIRRI-ICSTSGGFPEPHLSWLENG------EELNAINTTVSQ 165
              ||      | |::|:  :|  | |::|  ||  | | :|            |  :   ||
Db       140 PSQPEILHQADF-LETEKLKMLGECVVRDSYPEGNVTWYKNGRVLQPVEEVVVNLRKVE 198

Qy       166 DPETELYAVSSKLDFNMT----TNHSFMCLIKY 194
              |   ||  :  ||| |        | | || :|
Db       199 NRSTGLFTWTSSLQYMPTKEDANAKFTCIVTY 230
```

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RESULT 14
BUTY_MOUSE
ID   BUTY_MOUSE     STANDARD;      PRT;   524 AA.
AC   Q62556; P97392;
DT   01-NOV-1997 (Rel. 35, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Butyrophilin precursor (BT).
GN   BTN1A1 OR BTN.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129; TISSUE=Mammary gland;
RX   MEDLINE=97148936; PubMed=8995761;
RA   Ogg S.L., Komaragiri M.V.S., Mather I.H.;
RT   "Structural organization and mammary-specific expression of the
RT   butyrophilin gene.";
RL   Mamm. Genome 7:900-905(1996).
RN   [2]
RP   SEQUENCE OF 39-487 FROM N.A.
RC   TISSUE=Mammary gland;
RX   MEDLINE=96125722; PubMed=8541302;
RA   Ishii T., Aoki N., Noda A., Adachi T., Nakamura R., Matsuda T.;
RT   "Carboxy-terminal cytoplasmic domain of mouse butyrophilin
RT   specifically associates with a 150-kDa protein of mammary epithelial
RT   cells and milk fat globule membrane.";
RL   Biochim. Biophys. Acta 1245:285-292(1995).
CC   -!- FUNCTION: MAY FUNCTION IN THE SECRETION OF MILK-FAT DROPLETS. IT
```

```
CC         MAY ACT AS A SPECIFIC MEMBRANE-ASSOCIATED RECEPTOR FOR THE
CC         ASSOCIATION OF CYTOPLASMIC DROPLETS WITH THE APICAL PLASMA
CC         MEMBRANE (BY SIMILARITY).
CC   -!- SUBUNIT: SEEMS TO ASSOCIATE WITH XANTHINE DEHYDROGENASE/OXIDASE.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN MAMMARY TISSUE AND SECRETED IN
CC         ASSOCIATION WITH THE MILK-FAT-GLOBULE MEMBRANE DURING LACTATION.
CC   -!- DEVELOPMENTAL STAGE: EXPRESSION INCREASES DURING THE LAST HALF OF
CC         PREGNANCY AND IS MAXIMAL DURING LACTATION.
CC   -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. BTN/MOG
CC         SUBFAMILY.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
```

```
DR   EMBL; U67065; AAB51034.1; -.
DR   EMBL; S80642; AAB35893.1; -.
DR   MGD; MGI:103118; Btnla1.
DR   InterPro; IPR001870; Gamma_carbxylse.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig-v.
DR   InterPro; IPR003877; SPRY.
DR   InterPro; IPR003878; SPRY_domain.
DR   Pfam; PF00047; ig; 1.
DR   Pfam; PF00622; SPRY; 1.
DR   SMART; SM00406; IGv; 1.
DR   SMART; SM00449; SPRY; 1.
KW   Transmembrane; Glycoprotein; Signal.
FT   SIGNAL        1     26       POTENTIAL.
FT   CHAIN        27    524       BUTYROPHILIN.
FT   DOMAIN       27    247       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    248    268       POTENTIAL.
FT   DOMAIN      269    524       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD     56     56       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    216    216       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CONFLICT     46     46       D -> DD (IN REF. 2).
FT   CONFLICT    117    117       V -> F (IN REF. 2).
FT   CONFLICT    191    191       E -> D (IN REF. 2).
FT   CONFLICT    210    210       R -> S (IN REF. 2).
FT   CONFLICT    363    363       V -> E (IN REF. 2).
FT   CONFLICT    408    408       T -> K (IN REF. 2).
FT   CONFLICT    413    414       SL -> FF (IN REF. 2).
FT   CONFLICT    420    423       PRRV -> LAEY (IN REF. 2).
FT   CONFLICT    492    509       DIPLSPLGEGCTSGDKDT -> GHSLVPAGGRLYFWRQRH
FT                                (IN REF. 2).
SQ   SEQUENCE   524 AA;  58406 MW;  333F4D2C7704480 CRC64;

Query Match             10.4%;  Score 119;  DB 1;  Length 524;
Best Local Similarity   23.8%;  Pred. No. 0.011;
Matches   44;  Conservative   34;  Mismatches   87;  Indels   20;  Gaps    7;

Qy    20 ATLSCGH--NVSVEELAQTRIVWQKEKKMVLTMMSGD----MNIWPEYKNR----TIFD 68
            |:||    ||
Db    47 AELTCGFSPNASSEYM--ELLMFRQTRSTAVLLYRDGQGEQEGQOMTEYRGRAILATAGL 103

Qy    69 ITNNLSIVILALRPSDEGTYECVVLKIYEKDAFKREHLAEVTLSVKADFPTPSISDFEIPT 128
Db   104 LDGRATLLIRDVRVSDQGEYRC--LFKDNDDFEE---AAVYLKVAAVGSDPQIS-MTVQE 157

Qy   129 SNIRIICSTSGGFPEPHILSWLENGEELNAINTTVSQDPETELYAVSSKLDFNMTTNHSF 188
Db   158 NGEMELECTSSGWYPEPQVQWRIGNREMLPSTSESKHNEEGLFTVAVSMIRDSSIKNM 217

Qy   189 MCLIK 193
Db   218 SCCIQ 222
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RESULT 15

ID   NCA1_XENLA     STANDARD;      PRT;   1088 AA.
AC   P16170;
DT   01-APR-1990 (Rel. 14, Created)
DT   01-APR-1990 (Rel. 14, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Neural cell adhesion molecule 1, large isoform precursor (N-CAM 180)
DE   [Contains: N-CAM 140].
GN   NCAM1.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90098871; PubMed=2481269;
RA   Krieg P.A., Sakaguchi D.S., Kintner C.R.;
RT   "Primary structure and developmental expression of a large
RT   cytoplasmic domain form of Xenopus laevis neural cell adhesion
RT   molecule (NCAM).";
RL   Nucleic Acids Res. 17:10321-10335(1989).
CC   -!- FUNCTION: THIS PROTEIN IS A CELL ADHESION MOLECULE INVOLVED IN
CC       NEURON-NEURON ADHESION, NEURITE FASCICULATION, OUTGROWTH OF
CC       NEURITES, ETC.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- ALTERNATIVE PRODUCTS: THE DIFFERENT TISSUE-SPECIFIC FORMS OF
CC       N-CAM ARE PRODUCED BY ALTERNATIVE SPLICING.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN NEURON AND IN PRESUMPTIVE NEURAL
CC       TISSUE.
CC   -!- DEVELOPMENTAL STAGE: THE MRNA ENCODING THIS LD-NCAM IS THE MAJOR
CC       TRANSCRIPT PRESENT IN BOTH MATERNAL RNA AND IN THE EMBRYO DURING
CC       EARLY NEURAL DEVELOPMENT.
CC   -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC   -!- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC   -!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
```

```
DR   EMBL; M25696; AAA49909.1; -.
DR   PIR; S09600; IJXLNL.
DR   HSSP; P52276; 1TLK.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 2.
DR   Pfam; PF00047; ig; 5.
DR   SMART; SM00060; FN3; 2.
DR   SMART; SM00408; IGc2; 5.
KW   Cell adhesion; Glycoprotein; Transmembrane; Repeat; Brain;
KW   Immunoglobulin domain; Alternative splicing; Signal.
FT   SIGNAL        1     19       SIGNAL.
FT   CHAIN        20   1088       NEURAL CELL ADHESION MOLECULE 1, LARGE
FT                                ISOFORM.
FT   TRANSMEM    706    723       POTENTIAL.
FT   DOMAIN      724   1088       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       20    705       EXTRACELLULAR (POTENTIAL).
FT   DOMAIN       34    100       IG-LIKE C2-TYPE DOMAIN 1.
FT   DOMAIN      129    193       IG-LIKE C2-TYPE DOMAIN 2.
FT   DOMAIN      225    289       IG-LIKE C2-TYPE DOMAIN 3.
FT   DOMAIN      316    386       IG-LIKE C2-TYPE DOMAIN 4.
FT   DOMAIN      413    480       IG-LIKE C2-TYPE DOMAIN 5.
FT   DOMAIN      512    589       FIBRONECTIN TYPE-III 1.
FT   DOMAIN      618    686       FIBRONECTIN TYPE-III 2.
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FT   DOMAIN      149    153    HEPARIN-BINDING (POTENTIAL).
FT   DOMAIN      158    162    HEPARIN-BINDING (POTENTIAL).
FT   DISULFID     41     93    PROBABLE.
FT   DISULFID    136    186    PROBABLE.
FT   DISULFID    232    282    PROBABLE.
FT   DISULFID    323    379    PROBABLE.
FT   DISULFID    420    473    PROBABLE.
FT   CARBOHYD     82     82    N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    219    219    N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    310    310    N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    341    341    N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    417    417    N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    443    443    N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    472    472    N-LINKED (GLCNAC...) (POTENTIAL).
FT   VARSPLIC    804   1049    MISSING (IN ISOFORM N-CAM 140).
SQ   SEQUENCE   1088 AA;  117778 MW;  62738B55B03F3E83 CRC64;

Query Match             10.1%;  Score 116.5;  DB 1;  Length 1088;
Best Local Similarity   24.0%;  Pred. No. 0.044;
Matches   43;  Conservative  31;  Mismatches  58;  Indels  47;  Gaps   9;

Qy     18 EVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEYKNRITFDITNNLSIYI 77
          | |  | :  : :    : | :  |        :|    : :|    || :  : :
Db    130 EDAVIICDVSSSIPSI---ITWRHKGKDVI--------------FKKDVRFVVLANNYLQI 173

Qy     78 LALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSISDFEI---PTSNIRR- 133
          :|||||||| |       |:|   : :|  :|| |      ::       PTSNIRR
Db    174 RGIKKTDEGTYRC-----EGRILARGEINYKDIQVIVNVP-PTIQAROLRVNATANMAES 227

Qy    134 -IICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFN-----MTTNH 186
          :||||| || ||| :|||||| : :|:            :|  || | ||     MTTNH
Db    228 VVLSCDADGFPDPEISWLKKGEPI---------EDGE-----EKISFNEDQSEMTIHH 271
```

OM protein - protein search, using sw model

```
                              GenCore version 4.5
                              Copyright (c) 1993 - 2000  Compugen Ltd.

Run on:        June 18, 2002, 11:43:32 ; Search time 26.58 Seconds
                                          (without alignments)
                                          1405.828 Million cell updates/sec

Title:         US-09-454-651B-23
Perfect score: 1149
Sequence:      1 GLSHFCSGVIHVTKEVKEVA.........LRVNQTFNWNTKQEHFPDN 216

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched:      562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters:     562222

Post-processing: Minimum Match 0%
Maximum DB seq length: 2000000000
Minimum DB seq length: 0
               Maximum Match 100%
               Listing first 45 summaries

Database :     SPTREMBL_19:*
               1: sp_archea:*
               2: sp_bacteria:*
               3: sp_fungi:*
               4: sp_human:*
               5: sp_invertebrate:*
               6: sp_mammal:*
               7: sp_mhc:*
               8: sp_organelle:*
               9: sp_phage:*
               10: sp_plant:*
               11: sp_rodent:*
               12: sp_virus:*
               13: sp_vertebrate:*
               14: sp_unclassified:*
               15: sp_rvirus:*
               16: sp_bacterial:*
               17: sp_archeap:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1118	97.3	288	6	O77684	O77684 macaca neme
2	1100	95.7	288	6	Q28499	Q28499 macaca mula
3	1085	94.4	288	6	Q9BDN6	Q9BDN6 cercocebus
4	1085	94.4	289	6	O28347	O28347 cercocebus
5	764	66.5	230	6	Q9n2i3	Q9n2i3 sus scrofa
6	762.5	66.4	297	6	Q9tt70	Q9tt70 sus scrofa
7	762.5	66.4	297	6	Q9BE99	Q9be99 sus scrofa
8	761	66.2	229	6	Q9TT71	Q9tt71 sus scrofa
9	743	64.7	292	6	Q9GMZ8	Q9gmz8 sus scrofa
10	743	64.7	292	6	O02758	O02758 felis silve
11	719	62.6	304	6	Q9QX1	Q9qx1 canis famil
12	717.5	62.4	296	6	Q9TQX1	Q9tqx1 canis famil
13	705	61.4	235	6	O46405	O46405 bos taurus
14	705	61.4	235	6	Q9tqs8	Q9tqs8 canis famil
15	603.5	52.5	321	11	O35187	O35187 rattus norv
16	602	52.4	290	11	O62680	O62680 rattus norv

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17       601.5    52.3    321    11    O62624    rattus norv
18       596      51.9    321    11    O55202    rattus norv
19       560      48.7    306    11    Q9R1Z9    mus musculu
20       350      30.5    174    6     Q9GMZ9    felis silve
21       349.5    30.4    173    6     Q95117    felis silve
22       255.5    22.2    212    11    Q61332    mus musculu
23       200.5    17.4    329    6     Q9XSX6    felis silve
24       200.5    17.4    332    6     Q9GMZ7    macaca neme
25       200.5    17.4    332    6     Q95116    felis silve
26       188.5    16.4    280    6     Q9TTF1    canis famil
27       188.5    16.4    296    6     O42404    gallus gall
28       182      15.8    329    6     Q9TTF2    canis famil
29       178      15.5    323    6     Q9BDM2    cercopithec
30       178      15.4    323    6     Q9BDM9    macaca neme
31       177      15.4    323    6     Q9BDM4    macaca mula
32       176      15.3    275    6     Q9BDN9    cercocebus
33       176      15.3    323    6     Q9BDN8    cercocebus
34       171      14.9    284    6     Q9GL33    bos taurus
35       162      14.1    313    11    O35531    rattus norv
36       161.5    14.1    325    6     O02838    sus scrofa
37       156.5    13.6    290    4     Q9NZQ7    homo sapien
38       153      13.3    290    11    Q9EP73    mus musculu
39       153      13.3    356    6     Q64381    mus musculu
40       152      13.2    314    11    Q61238    mus musculu
41       150      13.1    309    11    Q91YV7    mus musculu
42       142      12.4    316    4     Q9BXR1    homo sapien
43       139.5    12.1    521    6     Q9BXR1    homo sapien
44       138      12.0    509    11    O46651    oryctolagus
45       137      11.9    509    11    P97710    rattus norv
                                        Q9QW15    rattus norv
```

ALIGNMENTS

```
RESULT   1
O77684
ID    O77684;          PRELIMINARY;     PRT;    288 AA.
AC    O77684;
DT    01-NOV-1998 (TrEMBLrel. 08, Created)
DT    01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT    01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE    B7 PROTEIN.
GN    B7.
OS    Macaca nemestrina (Pig-tailed macaque).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC    Cercopithecinae; Macaca.
OX    NCBI_TaxID=9545;
RN    [1]
RP    SEQUENCE FROM N.A.
RA    Kraus G., Hnatyszyn J.H.;
RL    Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
DR    EMBL; AF079519; AAC31555.1; 1.
DR    InterPro; IPR003599; Ig.
DR    InterPro; IPR003600; Ig_like.
DR    InterPro; IPR003006; Ig_MHC.
DR    Pfam; PF00047; ig; 1.
DR    SMART; SM00409; IG_like; 1.
DR    SMART; SM00410; IG_like; 1.
SQ    SEQUENCE  288 AA;  33131 MW;  76BBC42839E9AB79 CRC64;
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Query Match        97.3%;    Score 1118;  DB 6;   Length 288;
Best Local Similarity   97.7%;    Pred. No. 4.6e-96;
Matches  210;  Conservative  1;  Mismatches  4;  Indels  0;  Gaps  0;

Qy      2  LSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEY   61
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     28  LSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEY   87

Qy     62  KNRTIFDITNNLSIVILALRPSDEGTYECVLKYEKDAFKREHLAEVTLSVKADFPTPSI  121
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     88  KNRTIFDITNNLSIVILALRPSDEGTYECVLKYEKDAFKREHLAEVMLSVKADFPTPSI  147
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Qy    122  SDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFN  181
           ||||||:||||||||||||||||||||||||||||||||||||||||||:|||||||||
Db    148  TDFEIPPSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYTVSSKLDFN  207

Qy    182  MTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN  216
           |||||||||||||||||||||||||||||||||||
Db    208  MTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN  242


RESULT 2
ID   Q28499          PRELIMINARY;      PRT;   288 AA.
AC   Q28499;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   B7 PROTEIN (CD80 PROTEIN PRECURSOR).
GN   B7 OR N939.
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BLOOD;
RX   MEDLINE=96003435; PubMed=7561102;
RA   Villinger F., Brar S.S., Mayne A., Chikkala N., Ansari A.A.;
RT   "Comparative sequence analysis of cytokine genes from human and
RT   nonhuman primates.";
RL   J. Immunol. 155:3946-3954(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA   Weiss W.R., Ansari A.A.;
RT   "Cloning, sequencing and homology analysis of nonhuman primate
RT   Fas/Fas-ligand and co-stimulatory molecules.";
RL   Immunogenetics 0:0-0(2001).
DR   EMBL; U19840; AAA86706.1; -.
DR   EMBL; AF344849; AAK37609.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00410; IG_like; 1.
FT   SIGNAL       1     26       POTENTIAL.
SQ   SEQUENCE    288 AA;  33141 MW;  E70BEA4006C7A609 CRC64;

Query Match             95.7%;  Score 1100;  DB 6;  Length 288;
Best Local Similarity   96.3%;
  Matches  207;  Conservative    2;  Mismatches    6;  Indels    0;  Gaps    0;
                                                      Pred. No. 2.2e-94;

Qy      2  LSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEY   61
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     28  LSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEY   87

Qy     62  KNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADPPTPSI  121
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     88  KNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADPPTPSI  147

Qy    122  SDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFN  181
           ||||||:||||||||||||||||||||||||||||||||||||||||||:|||||||||
Db    148  TDFEIPPSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYTVSSKLDFN  207

Qy    182  MTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN  216
           |||||||||||||||||||||||||||||||||||
Db    208  MTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN  242


RESULT 3
ID   Q9BDN6          PRELIMINARY;      PRT;   288 AA.
AC   Q9BDN6;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   CD80 PROTEIN.
GN   MNB71.
OS   Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Cercocebus.
OX   NCBI_TaxID=9531;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21383618; PubMed=11491535;
RA   Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA   Weiss W.R., Ansari A.A.;
RT   "Cloning, sequencing, and homology analysis of nonhuman primate
RT   Fas/Fas-ligand and co-stimulatory molecules.";
RL   Immunogenetics 53:315-328(2001).
DR   EMBL; AF344839; AAK37535.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00410; IG_like; 1.
SQ   SEQUENCE    288 AA;  32917 MW;  C6A3F6A3C592972B CRC64;

Query Match             94.4%;  Score 1085;  DB 6;  Length 288;
Best Local Similarity   95.3%;
  Matches  205;  Conservative    4;  Mismatches    6;  Indels    0;  Gaps    0;
                                                      Pred. No. 5.4e-93;

Qy      2  LSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEY   61
           ||||||||||||||||||||||||||||||||||||||:|||||||||||||:|||||||
Db     28  LSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYCQKEKKMVLTMISGDMNIWPEY   87

Qy     62  KNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADPPTPSI  121
           |||||||||||||||||||||||||||||:|||||||||||||||:||||||||||||||
Db     88  KNRTIFDITNNLSIVILALRPSDEGTYECVLKYEKDAFKREHLAEVMLSVKADPPTPSI   147

Qy    122  SDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFN  181
           ||||||:|||||||||||||||||||||||||||||:||||||||||||||:|||||||||
Db    148  TDFEIPPSNIRRIICSTSGGFPEPHLSWLENGEELNAIDTTVSQDPETELYTVSSKLDFN  207

Qy    182  MTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN  216
           ||||||:||||||||||||||||||||||||||||
Db    208  MTTNHSFVCLIKYGHLRVNQTFNWNTTKQEHFPDN  242


RESULT 4
ID   Q28347          PRELIMINARY;      PRT;   289 AA.
AC   Q28347;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   B7 PROTEIN (FRAGMENT).
GN   B7.
OS   Cercocebus torquatus (red-crowned mangabey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Cercocebus.
OX   NCBI_TaxID=9530;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BLOOD;
RX   MEDLINE=96003435; PubMed=7561102;
RA   Villinger F., Brar S.S., Mayne A., Chikkala N., Ansari A.A.;
RT   "Comparative sequence analysis of cytokine genes from human and
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RT   nonhuman primates.";
RL   J. Immunol. 155:3946-3954(1995).
DR   EMBL; U19833; AAA86700.1; -.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00410; IG_like; 2.
FT   NON_TER     289     289
SQ   SEQUENCE   289 AA;  33030 MW;  5ED6A3F6A3C59297 CRC64;

Query Match             94.4%;  Score 1085;  DB 6;  Length 289;
Best Local Similarity   95.3%;
Matches  205;  Conservative    4;  Mismatches    6;  Indels    0;  Gaps    0;  Pred. No. 5.4e-93;

Qy      2  LSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEY  61
           |||||||||||||||||||||||||||||||||||||| ||||||||::|||||||||||
Db     28  LSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYCQKEKKMVLTMSGDMNIWPEY   87

Qy     62  KNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSI  121
           ||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db     88  KNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVMLSVKADFPTPSI  147

Qy    122  SDFEIPTSNIRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFN  181
           :|||||::||| ||||||||||||||||||||||||| |||||||||||||:|||||| |
Db    148  TDFEIPPSNIRRIICSTSGGFPEPHLSWLENGGEELNAIDTTVSQDPETELYTVSSKLDEN 207

Qy    182  MTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN  216
           |||||||:|||||||||||||||||||:|||||||
Db    208  MTTNHSFVCLIKYGHLRVNQTFNWNTPKQEHFPDN  242


RESULT   5

Q9N2I3     PRELIMINARY;     PRT;     230 AA.
ID   Q9N2I3
AC   Q9N2I3;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   CD80 PROTEIN PRECURSOR.
GN   CD80/B7.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=LANDRACE; TISSUE=SPLEEN;
RA   Wada M., Amae S., Hoshi M., Nio M., Ohi R.;
RT   "Porcine CD80(B-7) mRNA, partial cds.";
RL   Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB026121; BAA90700.2; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00410; IG_like; 1.
KW   Signal.
FT   SIGNAL      1      29
FT   CHAIN      30     230     POTENTIAL.
SQ   SEQUENCE   230 AA;  26028 MW;  EB63AD172663C4A4 CRC64;

Query Match             66.5%;  Score 764;  DB 6;  Length 230;
Best Local Similarity   67.0%;  Pred. No. 3e-63;
Matches  140;  Conservative    26;  Mismatches    43;  Indels    0;  Gaps    0;

Qy      1  GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE  60
           || ||||| : ||| ||| ||||| :| ::||| :| ||||| :::||| :||| | |||
Db     22  GLFDFCSGIVQVTKTVKEIAVLSCDYNISTEELTRVRIYWQKDNEMVLAVMSGKVKVWPK  81

Qy     61  YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS  120
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Db     82  YENRTFTDVTINNLCIVILALRLSDNGTYTCVVQKRERGSYKLEHLTSVKLMVKADPPVPS 141

Qy    121  ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF  180
Db    142  ITALGNPSPNIKRIRCSTSGGFPEPHLSWLENGEELNATNTMLSQDPETELYMISSELDF  201

Qy    181  NMTTNHSFMCLIKYGHLRVNQTFNWNTTK  209
Db    202  NVTGNHSFMCLVKYGGLTVSQTFNWQKCK  230


RESULT   6

Q9TT70     PRELIMINARY;     PRT;     288 AA.
ID   Q9TT70;
AC   Q9TT70;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   CD80 PROTEIN PRECURSOR (FRAGMENT).
GN   CD80.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20302785; PubMed=10843688;
RA   Faas S.J., Giannoni M.A., Mickle A., Kiesecker C.L., Reed D.J., Wu D.,
RA   Fodor W.L., Mueller J.P., Matis L.A., Rother R.P.;
RT   "Primary Structure and Functional Characterization of a Soluble,
RT   Alternatively Spliced Form of B7-1.";
RL   J. Immunol. 164:6340-6348(2000).
DR   EMBL; AF203443; AAF22750.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00410; IG_like; 1.
KW   Signal.
FT   SIGNAL      1      29
FT   CHAIN      30    >288
FT   NON_TER   288     288          CD80 PROTEIN.
SQ   SEQUENCE   288 AA;  32510 MW;  67E31D0FDB45D1C8 CRC64;

Query Match             66.4%;  Score 762.5;  DB 6;  Length 288;
Best Local Similarity   66.5%;  Pred. No. 5.6e-63;
Matches  141;  Conservative    28;  Mismatches    42;  Indels    1;  Gaps    1;

Qy      1  GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE  60
Db     22  GLFDFCSGIVQVTKEIAVLSCDYNISTEELTRVRIYWQKDNEMVLAVMSGKVKVWPK   81

Qy     61  YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS  120
Db     82  YENRTFTDVTNTNLCIVILALRLSDNGTYTCVVQKERGSYKLEHLTSVKLMVKADFPVPS  141

Qy    121  ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF  180
Db    142  ITALGNPSPNIKRIRCSTSGGFPEPHLSWLENGEELNATNTMLSQDPETELYMISSELDF  201

Qy    181  NMTTNHSFMCLIKYGHLRVNQTFNW-NTTKQE  211
Db    202  NVIGNHSFMCLVKYGGLTVSQTFNWQKSAKRE  233


RESULT   7

Q9BE99     PRELIMINARY;     PRT;     297 AA.
ID   Q9BE99;
AC   Q9BE99;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
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DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   CD80 PROTEIN PRECURSOR.
GN   CD80/B7-1.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=LANDRACE; TISSUE=ILEUM MUCOSA;
RA   Wada M., Amae S., Sano N., Ishii T., Hoshi M., Sasaki H., Nio M.,
RA   Hayashi Y., Ohi R.;
RT   "cloning and sequencing of cDNAs for porcine B7-1 (CD80) and soluble
RT   isoforms.";
RL   Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB049760; BAB40952.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00410; IG_like; 1.
KW   Signal.
FT   SIGNAL        1     29       POTENTIAL.
FT   CHAIN        30    297       CD80 PROTEIN.
SQ   SEQUENCE   297 AA;  33438 MW;  23I09711EA63EF23 CRC64;

Query Match      Best Local Similarity   66.4%;   Score 762.5;   DB 6;   Length 297;
                                         66.5%;   Pred. No. 5.8e-63;
Matches 141;   Conservative 28;   Mismatches 42;   Indels 1;   Gaps 1;

Qy     1  GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE   60
             |||| ||| || :|||  |||||||||:||||||::|||||||  |||::||::|||
Db    22  GLFDFCSGIVQVTKTVKEIAVLSCDYNISTEELTRVRIYWQKDNEMVLAVMSGKVKVWPK   81

Qy    61  YKNRTIFDITNNLSIVILALRPSDEGTIYECVLKYEKDAFKREHLAEVTLSVKADPFTPS  120
             |||||||| |||||||||||||||| ||| || |||:|||  :|:|||||| || ||
Db    82  YENRTFTDVTNNLCIVILALRLSDNGTYTCVVQKRERGSYKLEHLTSVKLMVKADFPVPS  141

Qy   121  ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF  180
             |: ||||||||  :||||||||||||||:|||||||||::|||||||||| |::|||
Db   142  ITALGNPSPNIKIRCSTSGGFPEPHLSWLENGEELNATNTMLSQDPETELYMISSELDF  201

Qy   181  NMTTNHSFMCLIKYGHLRVNQTFNW-NTTKQE                            211
             |::||||||| :|||| ||||| |  |:|
Db   202  NVTGNHSFMCLVKYGGLTVSQTFNW-QKSAKRE                           233


RESULT 8
Q9TT71

ID   Q9TT71;      PRELIMINARY;   PRT;   229 AA.
AC   Q9TT71;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   CD80 PROTEIN PRECURSOR.
GN   CD80 OR CD80/B7-1.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Faas S.J., Giannoni M.A., Mickle A., Kiesecker C.L., Reed D.J., Wu D.,
RA   Fodor W.L., Meuller J.P., Matis L.A., Rother R.P.;
RT   "Primary Structure and Functional Characterization of a Soluble,
RT   Alternatively Spliced Form of B7-1.";
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=SPLEEN;
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RA   Wada M., Amae S., Hoshi M., Nio M., Ishii T., Sano N., Sasaki H.,
RA   Ohi R.;
RT   "Splicing Isoform of Porcine CD80.";
RL   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF203442; AAF22749.1; -.
DR   EMBL; AB038153; BAA90764.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00410; IG_like; 1.
KW   Signal.
FT   SIGNAL        1     29
FT   CHAIN        30    229       CD80 PROTEIN.
SQ   SEQUENCE   229 AA;  25900 MW;  C3AD172663C4A4ED CRC64;

Query Match      Best Local Similarity   66.2%;   Score 761;   DB 6;   Length 229;
                                         67.8%;   Pred. No. 5.7e-63;
Matches 139;   Conservative 26;   Mismatches 40;   Indels 0;   Gaps 0;

Qy     1  GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE   60
             |||| ||| || :|||  |||||||||:||||||::|||||||  |||::||::|||
Db    22  GLFDFCSGIVQVTKTVKEIAVLSCDYNISTEELTRVRIYWQKDNEMVLAVMSGKVKVWPK   81

Qy    61  YKNRTIFDITNNLSIVILALRPSDEGTIYECVLKYEKDAFKREHLAEVTLSVKADPFTPS  120
             |||||||| |||||||||||||||| ||| || |||:|||  :|:|||||| || ||
Db    82  YENRTFTDVTNNLCIVILALRLSDNGTYTCVVQKRERGSYKLEHLTSVKLMVKADFPVPS  141

Qy   121  ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF  180
             |: ||||||||  :||||||||||||||:|||||||||::|||||||||| |::|||
Db   142  ITALGNPSPNIKIRCSTSGGFPEPHLSWLENGEELNATNTMLSQDPETELYMISSELDF  201

Qy   181  NMTTNHSFMCLIKYGHLRVNQTFNW-NTTKQE                            205
             |::||||||| :|||| ||||| |  |:|
Db   202  NVTGNHSFMCLVKYGGLTVSQTFNW-QKSAKRE                           226


RESULT 9
Q9GMZ8

ID   Q9GMZ8;      PRELIMINARY;   PRT;   292 AA.
AC   Q9GMZ8;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   B-LYMPHOCYTE ACTIVATION ANTIGEN B7-1 (CD80).
GN   CD80.
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20485322; PubMed=11029611;
RA   Nishimura Y., Shimojima M., Miyazawa T., Sato E., Nakamura K.,
RA   Izumiya Y., Ikeda Y., Mikami T., Takahashi E.;
RT   "Molecular cloning of the cDNA encoding the feline B-lymphocyte
RT   activation antigen B7-1 (CD80) and B7-2 (CD86) homologues which
RT   interact with human CTLA4-Ig.";
RL   Eur. J. Immunogenet. 27:427-430(2000).
DR   EMBL; AB030651; BAB11687.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00410; IG_like; 2.
SQ   SEQUENCE   292 AA;  33540 MW;  ED9AEECE10D30401 CRC64;

Query Match      Best Local Similarity   64.7%;   Score 743;   DB 6;   Length 292;
                                         63.3%;   Pred. No. 3.7e-61;
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Matches 136; Conservative 33; Mismatches 44; Indels 2; Gaps 1;

RESULT 10
ID   O02758;   PRELIMINARY;   PRT;   292 AA.
AC   O02758;
DT   01-JUL-1997 (TrEMBLrel. 04, Created)
DT   01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   T-CELL SPECIFIC SURFACE GLYCOPROTEIN B7-1.
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Hash S.M., Collisson E.W.;
RT   "Felis catus t-cell specific surface glycoprotein B7-1.";
RL   Thesis (1996), Veterinary Pathobiology, Texas A&M Univ.
DR   EMBL; U57755; AAB53575.1; -.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00410; IG_like; 2.
SQ   SEQUENCE   292 AA;   33482 MW;   6F117E7852B7950F CRC64;

Query Match   64.7%;   Score 743;   DB 6;   Length 292;
Best Local Similarity   63.3%;   Pred. No. 3.7e-61;
Matches 136; Conservative 33; Mismatches 44; Indels 2; Gaps 1;

Qy   2 LSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEY 61
         |||:|:||:| |||||||||||||||:||||:||||||:||:|||||||:||||||:|
Db   28 LFYFCSGIIQVNKTVEEVAVLSCDYNISTKELTEIRIYWQKDDEMVLAVMSGKYQVWPKY 87

Qy   62 KNRTFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADPPTPSI 121
         |||| |:|:| |||||||||||||||||||| |||:||:|||||||:||||||:|
Db   88 KNRTFDVTDNHSIVIMALRLSDNGKYTCIIQKIEKGSYXVKHLTSVMLLVRADPPVPSI 147

Qy   122 SDFEIPTSNIRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFN 181
         :| |:|:|||||||||||||||||||||||||||||||||||||||||:||:||||||
Db   148 TDLGNPSHNIKRIMCLTSGGFPKPHLSWLENEEELNAINTTVSQDPETELYTISSELDFN 207

Qy   182 MTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
         ||||||| ::||:|:|||| |:| |||:
Db   208 MTNNHSFLCLVKYGNLLVSQIFNWQ--KSEPQPSN 240

RESULT 11
ID   Q9TQX1;   PRELIMINARY;   PRT;   304 AA.
AC   Q9TQX1;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   B7-1 PROTEIN PRECURSOR.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20039996; PubMed=10630300;
RA   Yang S., Sim G.-K.;
RT   "New forms of Dog CD80 and CD86 Transcripts that Encode Secreted B7
RT   Molecules.";
RL   Immunogenetics 50:349-353(1999).
DR   EMBL; AF106824; AAF17293.1; -.
DR   EMBL; AF106829; AAF17293.1; JOINED.
DR   EMBL; AF106830; AAF17293.1; JOINED.
DR   EMBL; AF106831; AAF17293.1; JOINED.
DR   EMBL; AF106832; AAF17293.1; JOINED.
DR   EMBL; AF106833; AAF17293.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00410; IG_like; 1.
FT   SIGNAL.
KW   Signal.
FT   SIGNAL   1   33   POTENTIAL.
FT   CHAIN   34   304   B7-1 PROTEIN.
SQ   SEQUENCE   304 AA;   34454 MW;   09E082F6BB06C94F CRC64;

Query Match   62.6%;   Score 719;   DB 6;   Length 304;
Best Local Similarity   60.5%;   Pred. No. 6.7e-59;
Matches 130; Conservative 36; Mismatches 49; Indels 0; Gaps 0;

Qy   2 LSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEY 61
         |||:|:||:| |||||||||||||||:||||:||||||:||:|||||||:||||||:|
Db   28 LFYFCSGIIQVNKTVKEVAVLSCDYNISTTELMKVRIYWQKDDEVLAVTSGQTKVWSKY 87

Qy   62 KNRTFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADPPTPSI 121
         |||| |:|:| |||||||||||||||||||| |||:||:|||||||:||||||:|
Db   88 ENRTFADFTNNLSIVIMALRLSDNGKYTCIVQKTEKRSYKVKHMTSVMLLVRADPPVPSI 147

Qy   122 SDFEIPTSNIRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFN 181
         :| |:||||||||||||||||||||||||||||||||||||||||||||:||:||||||
Db   148 TDLGNPSHDIKRIMCSTSGGFPKPHLSWWENEEELNAANTTVSQDPETELYTISSELDFN 207

Qy   182 MTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
         ||||||| ::||:|:|||| |:| |||:
Db   208 ITSNHSFVCLVKYGDLIVSQIFNWQKSVEPHPNN 242

RESULT 12
ID   O46405;   PRELIMINARY;   PRT;   296 AA.
AC   O46405;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   CD80 ANTIGEN PRECURSOR (FRAGMENT).
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99115507; PubMed=9914337;
RA   Parsons K.R., Howard C.J.;
RT   "Cloning of cattle CD80.";
RL   Immunogenetics 49:231-234(1999).
DR   EMBL; Y09950; CAA71081.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003600; Ig_like.

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DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00410; IG_like; 1.
KW   Signal.
FT   SIGNAL        1     25
FT   NON_TER     296    296
SQ   SEQUENCE   296 AA;  33618 MW;  7ADB11FBF532EF5 CRC64;          POTENTIAL.

Query Match             63.2%;  Score 717.5;  DB 6;  Length 296;
Best Local Similarity   62.4%;
Matches  134;  Conservative   28;  Mismatches   47;  Indels    3;  Gaps    2;

Qy     1 GLSHFCSGVI--HVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIW  58
           ||  |||||    |:  |||||| :||||||  | :|||||||||| :||||||   |
Db    27 GLFYFCSGITPKSYVTKRVKETVMLSCDYNISTEELTSLRIYWQKDSKMVLIAILPGKVQVW  86

Qy    59 PEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYE-KDAFKREHLAEVTLSVKRADFP  117
          |||||||| :  |  |:||||| | || ||| |  :  | | ||||| | :| ||||
Db    87 PEYKNRTIFDMDNDNPRIVILALRLSDSGTYVCVIQKPDLKGAYKLEHLTSVRLMIRADFP  146

Qy   118 TPSISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSK  177
          :|:||  |||||||:| ||||||||||  || |||||||||||| ||||||| | :||
Db   147 VPTINDLGNPSPNIRRLICSTSGGFPPHLYWLENGEELNAINTTLSQDPETKLIYMISSE  206

Qy   178 LDFNMTTNHSFMCLIKYGHLRVNQTFNWNTTK  209
          |||||| ||||  || ||||:| |  |  |
Db   207 LDFNMTSNHSFPLCLVKYGDLTVSQIFYWQESK  238

RESULT 13
Q9TQS8
ID   Q9TQS8      PRELIMINARY;      PRT;   235 AA.
AC   Q9TQS8;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   SECRETED B7-1 PROTEIN PRECURSOR.
GN   CD80.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20093996; PubMed=10630300;
RA   Yang S., Sim G.-K.;
RT   "New Forms of Dog CD80 and CD86 Transcripts that Encode Secreted B7
RT   Molecules.";
RL   Immunogenetics 50:349-353(1999).
DR   EMBL; AF106825; AAF17296.1; -.
DR   EMBL; AF106831; AAF17294.1; -.
DR   EMBL; AF106829; AAF17294.1; JOINED.
DR   EMBL; AF106830; AAF17294.1; JOINED.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00410; IG_like; 1.
FT   SIGNAL        1     33
FT   CHAIN        34    235
SQ   SEQUENCE   235 AA;  26917 MW;  CC08CAA676BCB40A CRC64;          POTENTIAL.

Query Match             61.5%;  Score 705;  DB 6;  Length 235;
Best Local Similarity   61.4%;
Matches  128;  Conservative   33;  Pred. No. 9.7e-58;  Mismatches   47;  Indels    0;  Gaps    0;

Qy     2 LSHFCSGVIHVTKEVKEVAFLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEY  61
          |:||||  |  ||| |||  |:| | :|  ||| |  |  | ||| :|||||  |  |
Db     2 LSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEY  61
```

```
RESULT 14
Q9N0T0
ID   Q9N0T0      PRELIMINARY;      PRT;   235 AA.
AC   Q9N0T0;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   T-CELL CO-STIMULATORY PROTEIN B7-1.
GN   B7-1.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Khatlani T., Ma Z., Onishi T.;
RT   "Cloning and Sequencing of canine cDNA encoding T-cell co stimulatory
RT   molecule B7-1.";
RL   Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF25653; AAF69006.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00410; IG_like; 1.
SQ   SEQUENCE   235 AA;  26933 MW;  C0EA51DA9FB224E3 CRC64;

Query Match             61.5%;  Score 705;  DB 6;  Length 235;
Best Local Similarity   61.4%;
Matches  128;  Conservative   33;  Pred. No. 9.7e-58;  Mismatches   47;  Indels    0;  Gaps    0;

Qy     2 LSHFCSGIIQVNKTVKEVAVLSCDYNISTTELMKVRIYWQKDDEVVLAVTSGQTKVWSKY  61
Db     2 LSHFCSGIIQVNKTVKEVAVLSCDYNISTTELMKVRIYWQKDDEVVLAVTSGQTKVWSKY  61

Qy    62 KNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKRADFPPPSI  121
Db    62 KNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKRADFPPPSI  121

Qy   122 SDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFN  181
Db   148 TDLGNPSHDIKRIMCSTSGGFPKPHLSWWENEEELNAANTIVSQDPDTELYTISSELDFN  207

Qy   182 MTTNHSFMCLIKYGHLRVNQTFNWNTTK  209
Db   208 ITSNHSFVCLVKYGDLTVSQIFNWQKCK  235

RESULT 15
O35187
ID   O35187      PRELIMINARY;      PRT;   321 AA.
AC   O35187;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   B7.1.
```

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GN   B7.1.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FISCHER;
RX   MEDLINE=99176848; PubMed=10078962;
RA   Visse E., Siesjo P., Widegren B., Sjogren H.O.;
RT   "Regression of intracerebral rat glioma isografts by therapeutic
RT   subcutaneous immunization with interferon-gamma, interleukin-7, or
RT   B7-1-transfected tumor cells.";
RL   Cancer Gene Ther. 6:37-44(1999).
DR   EMBL; AF010465; AAB66351.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00410; IG_like; 1.
SQ   SEQUENCE   321 AA;  36351 MW;  071C6007FBBD1E60 CRC64;

Query Match             52.58;  Score 603.5;  DB 11;  Length 321;
Best Local Similarity   54.9%;  Pred. No. 4.1e-48;
Matches  113;  Conservative  34;  Mismatches  58;  Indels   1;  Gaps  1;

Qy     1 GLSHFCSGVI-HVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWP   59
           ||  |:| |:|||| | |||| :     |||:|||||||||||| ||||:||   ::||
Db    31 GLFQISSGIVGQVSKSVREKALLSCDYKFCSEEQSIHRIYWQKHDKMVLSVISGVPEVWP   90

Qy    60 EYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTP  119
          |||||:|||:|||||:|::|   |||||||:|   |:||| |:|||||||:||||||||
Db    91 EYKNRIVYDIANNYSFSLLGLILSDRGTYTCVVQRYEGESYVVKHLTTVELSVRADFPTP  150

Qy   120 SISDFEIPTSNIRRICSTSCGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD  179
           :|:: |    |:::::||  | |||||||    ||||:|||||||||:|||:|:|:||
Db   151 NITESGNPSADIKRTCFASGGFPKPRLSWLENGRELNGINTTISQDPESELYTISSQLD  210

Qy   180 FNMTTNHSFMCLIKYGHLRVNQTFNW  205
          ||:| ||:| ||:|  |:| | |
Db   211 FNTTYDHFIDCFIEYGDAHVSQNFTW  236

Search completed: June 18, 2002, 11:47:24
Job time: 232 sec
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OM protein - protein search, using sw model

                    GenCore version 4.5
                    Copyright (c) 1993 - 2000 Compugen Ltd.

Run on:             June 18, 2002, 11:43:07 ; Search time 29.83 Seconds
                                             (without alignments)
                                             804.289 Million cell updates/sec

Title:              US-09-454-651B-23
Perfect score:      1149
Sequence:           1 GLSHFCSGVIHVTKEVKEVA.........LRVNQTFNWNTTKQEHPPDN 216
Scoring table:      BLOSUM62
                    Gapop 10.0 , Gapext 0.5
Searched:           747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters:   747574

                    Listing first 45 summaries

Post-processing:    Minimum Match 100%
Maximum DB seq length: 200000000
Minimum DB seq length: 0

Database :          A_Geneseq_032802:*
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                 2: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
                 3: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1982.DAT:*
                 4: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1983.DAT:*
                 5: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1984.DAT:*
                 6: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1985.DAT:*
                 7: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1986.DAT:*
                 8: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1987.DAT:*
                 9: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1988.DAT:*
                10: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1989.DAT:*
                11: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1990.DAT:*
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SUMMARIES

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Result           %       Query
No.     Score   Match   Length   DB ID        Description
-----   -----   -----   ------   -----        -----------
  1     1149    100.0    288     AAR67989     Human B lymphocyte
  2     1149    100.0    288     AAW38414     B7-1, Homo sapien
  3     1149    100.0    288     AAW67804     Human B7 protein s
  4     1149    100.0    288     AAW73640     Human B7-2 antigen
  5     1149    100.0    288     AAB37087     Human B lymphocyte
  6     1149    100.0    288     AAY99966     Human B7 protein.
  7     1149    100.0    288     AAY44289     Human B7.1 co-stim
  8     1149    100.0    288     AAY54920     Human B7.1 protein
  9     1149    100.0    288     AAU05121     Colorectal tumour
 10     1149    100.0    288     AAI19959     Human B lymphocyte
 11     1149    100.0    473     AAW41415     Human B7.1-murine
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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ALIGNMENTS

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RESULT   1
AAR67989
ID    AAR67989 standard; Protein; 288 AA.
XX
AC    AAR67989;
XX
DT    21-AUG-1995 (first entry)
XX
DE    Human B lymphocyte antigen B7-1 (hB7-1).
XX
KW    B lymphocyte antigen; B7-1; B cell activation antigen; CD28;
KW    ligand; T cell surface antigen; transmembrane protein.
OS    Homo sapiens.
XX
FH    Key         Location/Qualifiers
FH
FT    Protein      1..34
FT                 /label= signal sequence
FT    Domain       35..242
FT                 /label= extracellular
FT    Domain       243..269
FT                 /label= transmembrane
FT    Domain       270..288
FT                 /label= intracellular
FT    Misc-difference  53..55
FT                 /label= N-linked glycosylation
FT    Misc-difference  89..91
FT                 /label= see above
FT    Misc-difference  98..100
FT                 /label= see above
FT    Misc-difference  186..188
FT                 /label= see above
FT    Misc-difference  207..209
FT                 /label= see above
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Alignment region (query vs subject):

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12    1146    99.7   251    20    AAW90208     hB7.lglu-glu solub
13    1144    99.6   475    18    AAW38415     Soluble B7-1 Ig.
14    1143    99.5   488    20    AAW86004     Human B7-1.5r4.1 P
15    1143    99.5   488    22    AAB83836     Amino acid sequenc
16    1143    99.5   492    19    AAW42338     CD80-Ig-alpha-tp f
17    1138    99.0   480    20    AAW90206     hB7.1Fc soluble fu
18    1047    91.1   208    18    AAW35858     Human B7.1 for use
19    761     66.2   229    22    AAY97780     Soluble porcine B7
20    743     64.7   292    21    AAY32283     Human B7.1
21    743     64.7   292    21    AAY32284     Feline CD80 (B7-1)
22    739     64.3   292    21    AAX32277     Cat CD80 (B7-1)-FA
23    739     64.3   304    20    AAY41077     Feline B7-1 protei
24    719     62.6   235    20    AAY41075     Canine B7-1 protei
25    705     61.4   292    21    AAX32276     Cat CD80 (B7-1)-SY
26    561     48.8   306    16    AAB82893     Canine B7-1 alterna
27    561     48.8   306    16    AAR67990     Murine B lymphocyt
28    561     48.8   320    16    AAB82892     Mouse B lymphocyte
29    561     48.8   306    22    AAB19960     Mouse B7-1 alterna
30    558     48.6   306    20    AAW67805     Mouse B7 protein s
31    558     48.6   306    20    AAW73641     Mouse B7-2 antigen
32    558     48.6   306    21    AAB37088     Mouse B lymphocyte
33    558     48.6   306    21    AAY99967     Murine B lymphocyt
34    349.5   30.4   173    20    AAY41082     Feline B7-1S prote
35    311     27.1   214    16    AAR82901     Mouse B7-1 (IgV-li
36    305     26.5   212    20    AAR82900     Mouse B7-1 (IgV-li
37    305     26.5   212    16    AAR82902     Mouse B7-1 (IgV-li
38    250.5   21.8   226    16    AAR82903     Mouse B7-1 IgV-lik
39    250.5   21.8   329    21    AAY32285     Feline CD86 (B7-2)
40    200.5   17.4   329    21    AAY32278     Cat CD86 (B7-2) li
41    200.5   17.4   332    20    AAY41079     Feline B7-2 protei
42    188.5   16.4   280    20    AAY41078     Canine B7-2 prote
43    182     15.8   244    20    AAW90209     hB7.1h1s soluble f
44    182     15.8   246    20    AAW86005     Human B7-2 extrace
45    182     15.8   246    22    AAB83837     Amino acid sequenc
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FT   Misc-difference 211..213
FT   /label= see above
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FT   /label= see above
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FT   /label= see above
FT   Domain   35..138
FT   /label= see above
FT   Domain   139..236
FT   /label= Ig V-set domain
FT   /label= Ig C-set domain
XX
PN   WO9503408-A.
XX
PD   02-FEB-1995.
XX
PF   26-JUL-1994; 94WO-US08423.
XX
PR   26-JUL-1993; 93US-0101624.
PR   19-AUG-1993; 93US-010393.
PR   03-NOV-1993; 93US-0147773.
XX
PA   (DAND) DANA FARBER CANCER INST INC.
PA   (REPK) REPLIGEN CORP.
XX
PI   Freeman GJ, Gray GS, Greenfield E, Nadler LM;
XX
DR   WPI; 1995-075236/10.
DR   N-PSDB; AAQ81371.
XX
PT   Nucleic acids encoding CTLA4/CD28 counter receptor, B7-2 - useful
PT   for enhancing or suppressing T-cell mediated immune responses
XX
PS   Disclosure; pages 111-113; 175pp; English.
XX
CC   Q81371 is in pCDM8 vector. It is derived from lymphoid B cells,
CC   cell line Raji, clone no. 13. Its position in the genome is
CC   chromosome/segment 3. It was published by Freeman, F.J. et al.,
CC   J. of Immunology; 143: 8: 2714-2722, 15th October 1989. It can be
CC   found in Genbank at Accession no. M27533. The encoded protein,
CC   R67989, binds both human CTLA4 and human CD28. It is related
CC   to human hB7-2 (see Q81351) and murine hB7 (see Q81372).
XX
SQ   Sequence   288 AA;

Query Match   100.0%; Score 1149; DB 16; Length 288;
Best Local Similarity 100.0%; Pred. No. 2.6e-103;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 27 glshfcsgvihvtkevkevatlscghnvsveelaqtriywqkekkmvltmmsgdmniwpe 86

Qy 61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 87 yknrtifditnnlsivilalrpsdegtyecvvlkyekdafkrehlaevtlsvkadfptps 146

Qy 121 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 147 isdfeiptsnirriicstsggfpephlswlengeelnainttvsqdpetelyavsskldf 206

Qy 181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
        ||||||||||||||||||||||||||||||||||||
Db 207 nmttnhsfmclikyghlrvnqtfnwnttkqehfpdn 242

RESULT 2
AAW38414
ID   AAW38414 standard; Protein; 288 AA.
XX
AC   AAW38414;
XX

DT   08-APR-1998   (first entry)
XX
DE   B7-1.
XX
KW   Screening; inhibitor; enhancer; binding; CD28; B7-1.
XX
OS   Homo sapiens.
XX
PN   EP795554-A2.
XX
PD   17-SEP-1997.
XX
PF   04-MAR-1997; 97EP-0301438.
XX
PR   02-OCT-1996; 96JP-0262085.
PR   05-MAR-1996; 96JP-0047795.
XX
PA   (TAKE) TAKEDA CHEM IND LTD.
XX
PI   Hattori M, Hida T, Kurokawa T, Nakanishi A;
XX
DR   WPI; 1997-450803/42.
DR   N-PSDB; AAT96358.
XX
PT   New xanthene derivatives useful as immunomodulators - e.g. methyl
PT   2-(carboxymethylsulphinyl)-5,7-dichloro-3,8-dihydroxy-6-
PT   methyl-9-oxo-9H-xanthene-1-carboxylate.
XX
PS   Disclosure; Fig 4; 117pp; English.
XX
CC   The present sequence was used in the development of a novel method
CC   for screening for compounds that inhibit or enhance binding of CD28
CC   to B7-1.
XX
SQ   Sequence   288 AA;

Query Match   100.0%; Score 1149; DB 18; Length 288;
Best Local Similarity 100.0%; Pred. No. 2.6e-103;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 27 glshfcsgvihvtkevkevatlscghnvsveelaqtriywqkekkmvltmmsgdmniwpe 86

Qy 61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 87 yknrtifditnnlsivilalrpsdegtyecvvlkyekdafkrehlaevtlsvkadfptps 146

Qy 121 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 147 isdfeiptsnirriicstsggfpephlswlengeelnainttvsqdpetelyavsskldf 206

Qy 181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
        ||||||||||||||||||||||||||||||||||||
Db 207 nmttnhsfmclikyghlrvnqtfnwnttkqehfpdn 242

RESULT 3
AAW67804
ID   AAW67804 standard; Protein; 288 AA.
XX
AC   AAW67804;
XX
DT   13-APR-1999   (first entry)
XX
DE   Human B7 protein sequence.
XX
KW   Human; B7; transfection; mammal; tumour cell; sarcoma; co-stimulation;
KW   T- cell; CD28; CTLA4; ligand; T-lymphocyte response; metastasis.
XX
OS   Homo sapiens.
XX

```
FH   Key             Location/Qualifiers
FT   Peptide         1..34
FT                   /note= "signal peptide"
FT   Protein         35..288
FT                   /note= "mature B7 protein"
FT   Domain          35..242
FT                   /note= "extracellular domain"
FT   Domain          243..269
FT                   /note= "transmembrane domain"
FT   Domain          270..288
FT                   /note= "intracellular domain"
FT   Modified-site   53..55
FT                   /note= "Asn is N-glycosylated"
FT   Modified-site   89..91
FT                   /note= "Asn is N-glycosylated"
FT   Modified-site   98..100
FT                   /note= "Asn is N-glycosylated"
FT   Modified-site   186..188
FT                   /note= "Asn is N-glycosylated"
FT   Modified-site   207..209
FT                   /note= "Asn is N-glycosylated"
FT   Modified-site   211..213
FT                   /note= "Asn is N-glycosylated"
FT   Modified-site   226..228
FT                   /note= "Asn is N-glycosylated"
FT   Modified-site   236..234
FT                   /note= "Asn is N-glycosylated"
FT   Modified-site   35..139
FT                   /note= "Asn is N-glycosylated"
FT   Domain          35..139
FT                   /note= "Ig V-set domain"
FT   Domain          140..236
FT                   /note= "Ig C-set domain"
XX
SQ   Sequence        288 AA;
```

Query Match   100.0%; Score 1149; DB 20; Length 288;
Best Local Similarity   100.0%; Pred. No. 2.6e-103;
Matches 216; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Qy          1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         27 glshfcsgvihvtkevkevatlscghnvsveelaqtriywqkekkmvltmmsgdmniwpe 86

Qy         61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPPPS 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         87 yknrtifditnnlsivilalrpsdegtyecvvlkyekdafkrehlaevtlsvkadfppps 146

Qy        121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 isdfeiptsnirriicstsggfpephlswlengeelnaintvsqdpetelyavsskldf 206

Qy        181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
              ||||||||||||||||||||||||||||||||||||
Db        207 nmttnhsfmclikyghlrvnqtfnwnttkqehfpdn 242
```

```
RESULT    4
AAW73640
ID   AAW73640 standard; Protein; 288 AA.
XX
AC   AAW73640;
XX
DT   23-MAR-1999  (first entry)
XX
DE   Human B7-2 antigen.
XX
KW   B7-2 antigen; mammalian tumour cell; T cell costimulation; CD28 ligand;
KW   CTLA4 ligand; therapy; T-cell response; human.
XX
OS   Homo sapiens.
XX
PN   US5861310-A.
XX
PD   19-JAN-1999.
XX
PF   30-MAY-1995;  95US-0456104.
PR   30-MAY-1995;  95US-0456104.
PR   03-NOV-1993;  93US-0147773.
XX
PA   (DAND ) DANA FARBER CANCER INST INC.
XX
PI   Freeman GJ, Gray GS, Nadler LM;
XX
DR   WPI; 1999-130394/11.
DR   N-PSDB; AAV55786.
XX
PT   Tumour cell transfected to express B7-2 molecule - useful for tumour
PT   therapy by stimulating T-cell response
XX
PS   Disclosure; Column 37-40; 27pp; English.
XX
CC   This sequence is the human B7-2 antigen, which can be used in the
CC   method of the invention. The method is for transfecting an isolated
CC   mammalian tumour cell with an exogenous nucleic acid molecule encoding a
CC   mammalian B7-2 molecule, where the B7-2 molecule is expressed in the
CC   tumour cell is capable of costimulating a T cell and is capable of
CC   binding a CD28 or CTLA4 ligand. The method is useful for treating tumours
CC   by stimulating a T-cell response against tumour cells in vivo.
XX
SQ   Sequence        288 AA;
```

Query Match   100.0%; Score 1149; DB 20; Length 288;
Best Local Similarity   100.0%; Pred. No. 2.6e-103;
Matches 216; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy          1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         27 glshfcsgvihvtkevkevatlscghnvsveelaqtriywqkekkmvltmmsgdmniwpe 86

Qy         61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPPPS 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         86 yknrtifditnnlsivilalrpsdegtyecvvlkyekdafkrehlaevtlsvkadfppps 120
```

```
Db   87 yknrtifditnnlsivlilalrpsdegtyecvvlkyekdafkrehlaevtlsvkadfpts 146
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  147 isdfeiptsnirriicstsggfpephlswlengeelnainttvsqdpetelyavsskldf 206

Qy  181 NMTTNHSFEMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
        |||||||||| ||||||||||||||||||||| |||||
Db  207 nmttnhsfmclikyghlrvnqtfnwnttkgehfpdn 242
```

RESULT 5

```
ID   AAB37087 standard; Protein; 288 AA.
XX
AC   AAB37087;
XX
DT   28-MAR-2001  (first entry)
XX
DE   Human B lymphocyte antigen B7-1.
XX
KW   Immunomodulator; fusion protein; human; murine; mouse; lymphocyte; CD28;
KW   antigen; extracellular domain; CTLA4; immunoglobulin constant region;
KW   immunogenicity; tumour; sarcoma; antigen presenting cell; macrophage;
KW   T cell-mediated immune response; transplantation; vaccination.
XX
OS   Homo sapiens.
XX
PN   US5130316-A.
XX
PD   10-OCT-2000.
XX
PF   26-JUL-1994;  94US-0280757.
XX
PR   26-JUL-1993;  93US-0101624.
PR   19-AUG-1993;  93US-0109393.
PR   03-NOV-1993;  93US-0147773.
XX
PA   (DAND ) DANA FARBER CANCER INST INC.
PA   (REPK ) REPLIGEN CORP.
XX
PI   Freeman GJ, Nadler LM, Gray GS, Greenfield E;
XX
DR   WPI; 2000-655681/63.
DR   N-PSDB; AAC84051.
XX
PT   Nucleic acids and fusion proteins of CTLA4/CD28 ligands, useful for
PT   enhancing or suppressing T cell-mediated immune responses, especially
PT   during tissue, skin or organ transplantation, or in graft-versus-host
PT   disease
```

PS   Disclosure: Column 87-90; 83pp; English.

```
CC   The invention relates to an isolated nucleic acid molecule encoding a
CC   fusion protein comprising a first nucleotide sequence encoding a first
CC   peptide, and a second nucleotide sequence encoding a second peptide.
CC   The first nucleotide sequence hybridizes in 6 X sodium chloride/sodium
CC   citrate (SSC) at 45 deg. C, followed by a wash in 0.2 X SSC at 50 deg. C
CC   to a portion of a nucleotide sequence which encodes a human or murine
CC   B lymphocyte antigen (B7-2) extracellular domain. The first peptide has
CC   the ability to bind CD28 or CTLA4. The first peptide has an amino acid
CC   sequence that is identical or at least 50% identical with the
CC   extracellular domain of a human B7-2 peptide (AAB37085). The second
CC   peptide is especially an immunoglobulin constant region. This sequence
CC   represents the human B lymphocyte antigen B7-1. The sequence is used for
CC   comparison with the B7-2 sequence. The human B7-2 protein is an example
CC   of a first peptide sequence of the invention. The nucleic acid molecules
CC   are useful in various expression vectors to direct synthesis of the
CC   corresponding proteins or peptides in a variety of hosts, particularly
CC   eukaryotic cells, e.g. mammalian or insect cell culture. The nucleic
CC   acids are also useful for enhancing the immunogenicity of a mammalian
CC   cell, e.g. tumour cell (sarcoma) or an antigen presenting cell
     ,
CC   (macrophage). The fusion proteins or peptides are useful for enhancing or
CC   suppressing T cell-mediated immune responses, e.g. in situations of
CC   tissue, skin or organ transplantation, or in graft-versus-host disease.
CC   The proteins are also useful for enhancing the efficacy of vaccination
CC   against a variety of pathogens, and may also be used to upregulate an
CC   immune response against a particular pathogen during an infection or
CC   against a tumour in a tumour-bearing host.
XX
SQ   Sequence 288 AA;
```

```
Qy  181 NMTTNHSFEMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
        |||||||||| ||||||||||||||||||||| |||||
Db  207 nmttnhsfmclikyghlrvnqtfnwnttkgehfpdn 242
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RESULT 6

```
ID   AAY99966 standard; Protein; 288 AA.
XX
AC   AAY99966;
XX
DT   10-JAN-2001  (first entry)
XX
DE   Human B7 protein.
XX
KW   B7; human; B cell activation antigen; B lymphocytes;
KW   autoimmune disease; rheumatoid arthritis; multiple sclerosis;
KW   herpes simplex; influenza; common cold; HIV.
XX
OS   Homo sapiens.
XX
```

```
Query Match             100.0%;  Score 1149;  DB 21;  Length 288;
Best Local Similarity   100.0%;  Pred. No. 2.6e-103;
Matches  216;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db   27 glshfcsgvihvtkevkevatlscghnvsveelaqtriywqkekkmvltmmsgdmnlwpe 86

Qy   61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
        |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||| |
Db   87 yknrtifditnnlsivlilalrpsdegtyecvvlkyekdafkrehlaevtlsvkadfpts 146

Qy  121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  147 isdfeiptsnirriicstsggfpephlswlengeelnainttvsqdpetelyavsskldf 206

Qy  181 NMTTNHSFEMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
        |||||||||| ||||||||||||||||||||| |||||
Db  207 nmttnhsfmclikyghlrvnqtfnwnttkgehfpdn 242
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FH   Key             Location/Qualifiers
FT   Peptide         1..34
FT                   /label= signal_peptide
FT   Domain          35..242
FT                   /label= Extracellular_domain
FT   Domain          35..138
FT                   /label= "Ig V-set domain"
FT   Modified-site   53..55
FT                   /note= "N-linked glycosylation site"
FT   Modified-site   89..91
FT                   /note= "N-linked glycosylation site"
FT   Modified-site   98..100
FT                   /note= "N-linked glycosylation site"
FT   Domain          139..236
FT                   /label= "Ig C-set domain"
FT   Modified-site   186..188
FT                   /note= "N-linked glycosylation site"
FT   Modified-site   207..209
FT                   /note= "N-linked glycosylation site"
FT   Modified-site   211..213
FT                   /note= "N-linked glycosylation site"
FT   Modified-site   226..228
FT                   /note= "N-linked glycosylation site"
FT   Modified-site   232..234
FT                   /note= "N-linked glycosylation site"
```

```
FT   Domain          243..269
FT                   /label= Transmembrane_domain
FT   Domain          270..288
FT                   /label= Intracellular_domain
XX
PN   US6071716-A.
XX
PD   06-JUN-2000.
XX
PF   15-NOV-1993;   93US-0153262.
XX
PR   28-AUG-1991;   91US-0751306.
PR   01-OCT-1990;   90US-0591300.
XX
PA   (DAND ) DANA FARBER CANCER INST INC.
XX
PI   Nadler LM, Freeman GJ, Freedman AS;
XX
DR   WPI; 2000-422081/36.
DR   N-PSDB; AAA61328.
XX
PT   New polynucleotides encoding a B7 activation antigen, useful for
PT   regulating T cell mediated immune responses or viral diseases -
XX
PS   Claim 1; Fig 4; 36pp; English.
XX
CC   The present sequence is the unique human B cell activation antigen B7
CC   protein. The cDNA encoding this sequence was isolated from a Burkitt
CC   lymphoma cell line cDNA library. Selection of cDNA clones was based
CC   on expression of B7, as detected by the anti-B7 monoclonal antibody.
CC   The human B7 cDNA was used in hybridisation analysis to isolate the
CC   murine B7 cDNA (see AAA61329). The B7 nucleic acid sequences may be
CC   used to generate transgenic, knock-out animals which, in turn, are
CC   useful in the development and screening of therapeutically useful
CC   reagents. The expressed B7 protein is useful for enhancing or
CC   blocking activated T cell mediated immune responses and immune
CC   function. Modification of B7 expression is useful in the treatment of
CC   autoimmune diseases (e.g. rheumatoid arthritis or multiple sclerosis),
CC   herpes simplex, influenza, the common cold and HIV. It is also useful
CC   in tissue and organ transplantation.
XX
SQ   Sequence   288 AA;

Query Match             100.0%;  Score 1149;  DB 21;  Length 288;
Best Local Similarity   100.0%;  Pred. No. 2.6e-103;
Matches  216;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy         1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        27 glshfcsgvihvtkevkevatlscghnvsveelaqtriywqkekkmvltmmsgdmniwpe 86

Qy        61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        87 yknrtifditnnlsivilalrpsdegtyecvvlkyekdafkrehlaevtlsvkadfptps 146

Qy       121 ISDFEIPTSNIRRICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       147 isdfeiptsnirriicstsggfpephlswlengeelnainttvsqdpetelyavsskldf 206

Qy       181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
             ||||||||||||||||||||||||||||||||||||
Db       207 nmttnhsfmclikyghlrvnqtfnwnttkqehfpdn 242


RESULT  7
AAY44289
ID   AAY44289 standard; protein; 288 AA.
XX
AC   AAY44289;
XX
DT   29-FEB-2000  (first entry)
XX
```

```
DE   Human B7.1 co-stimulatory molecule.
XX
KW   Human B7.1 co-stimulatory molecule; antigen presenting cell;
KW   immune response; cell surface receptor; Major histocompatibility complex;
KW   MHC classII; proton motor force; mitochondrial membrane potential;
KW   mitochondrial metabolism; cancer; autoimmune disease; glycoprotein;
KW   neurodegenerative disorder.
XX
OS   Homo sapiens.
XX
PN   WO9953953-A2.
XX
PD   28-OCT-1999.
XX
PF   30-MAR-1999;   99WO-US06874.
XX
PR   17-APR-1998;   98US-0082250.
PR   29-JUL-1998;   98US-0094519.
PR   24-SEP-1998;   98US-0101580.
XX
PA   (UVVE-) UNIV VERMONT.
XX
PI   Newell MK;
XX
DR   WPI; 2000-096773/08.
DR   N-PSDB; AAZ29320.
XX
PT   Use of cell surface and membrane characteristics for developing
PT   products for treating cancers, autoimmune diseases or neurodegenerative
PT   diseases -
XX
PS   Disclosure; Page 115; 123pp; English.
XX
CC   The present sequence is human B7.1 co-stimulatory molecule. This is
CC   a glycoprotein on the surface of antigen presenting cells. This is
CC   involved in stimulation of an immune response by its ability to interact
CC   with various immune cell surface receptors. The regulation of cell
CC   surface expression of MHC classII and co-stimulatory molecule B7 can be
CC   manipulated by regulating the intracellular dissipation of proton motor
CC   force which can be assessed in terms of mitochondrial membrane potential.
CC   These methods can be used for regulating cell growth and division to
CC   control disease processes by manipulating mitochondrial metabolism and
CC   the expression of cell surface immune proteins. They can be used for
CC   treating diseases associated with excessive cellular death, aberrant
CC   differentiation, and premature cellular death, e.g. cancers, autoimmune
CC   diseases, neurodegenerative disorders etc.
XX
SQ   Sequence   288 AA;

Query Match             100.0%;  Score 1149;  DB 21;  Length 288;
Best Local Similarity   100.0%;  Pred. No. 2.6e-103;
Matches  216;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy         1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        27 glshfcsgvihvtkevkevatlscghnvsveelaqtriywqkekkmvltmmsgdmniwpe 86

Qy        61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        87 yknrtifditnnlsivilalrpsdegtyecvvlkyekdafkrehlaevtlsvkadfptps 146

Qy       121 ISDFEIPTSNIRRICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       147 isdfeiptsnirriicstsggfpephlswlengeelnainttvsqdpetelyavsskldf 206

Qy       181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
             ||||||||||||||||||||||||||||||||||||
Db       207 nmttnhsfmclikyghlrvnqtfnwnttkqehfpdn 242


RESULT  8
AAY54920
```

```
ID   AAY54920 standard; Protein; 288 AA.
XX
AC   AAY54920;
XX
DT   14-FEB-2000  (first entry)
XX
DE   Human B7.1 protein sequence.
XX
KW   Interleukin-12; IL-12; fusion protein; IL-12 p35 subunit; B7 protein;
KW   IL-12 p40 subunit; gene therapy; tumour; leukaemia; B7.1 protein.
XX
OS   Homo sapiens.
XX
PN   US5994104-A.
XX
PD   30-NOV-1999.
XX
PF   08-NOV-1996;   96US-0751767.
XX
PR   08-NOV-1996;   96US-0751767.
XX
PA   (UNLO ) ROYAL FREE HOSPITAL SCHOOL MED.
XX
PI   Anderson RJ, Prentice HG, MacDonald ID;
XX
DR   WPI; 2000-038261/03.
DR   N-PSDB; AA240022.
XX
PT   Nucleic acid constructs encoding interleukin-12 fusion proteins useful
PT   for treating leukemia and other cancers -
XX
PS   Example: Fig 10; 73pp; English.
XX
CC   This sequence represents the human B7.1 protein sequence.
CC   The invention relates to an isolated nucleic acid construct (I)
CC   comprising a region encoding an interleukin-12 (IL-12) fusion protein
CC   (comprising an IL-12 p35 subunit, an IL-12 p40 subunit and a linker
CC   peptide (joining the subunits)) and a region encoding a B7 protein. (I)
CC   may be used to produce IL-12 fusion proteins according to standard
CC   recombinant DNA methodologies. The fusion proteins may be produced either
CC   in vitro in a fermentation culture or in vivo as part of a gene therapy
CC   protocol (in this case (I) is used to transform a patients cells, which
CC   then secrete the functional polypeptide to supplement the patients own
CC   production of IL-12 or to rectify mutations which lead to the expression
CC   of inactive polypeptides). The fusion proteins produced in this way may
CC   be used to treat any disease which responds to IL-12 such as tumours
CC   (both solid and dispersed of the kidney, breast, colon, ovarian and
CC   cervical tumours and melanomas) and in particular, tumours of the blood
CC   such as leukaemia. Alternatively, the polypeptides may be used as
CC   antigens in the production of antibodies to IL-12 and to assay for
CC   agonists and antagonists of its activity. The antibodies and antagonists
CC   may be used to inhibit the activity of IL-12. (I) may also be used
CC   diagnostically as a probe which hybridizes to sequences encoding IL-12
CC   and the antibodies may be used to detect the presence of IL-12
CC   polypeptides in samples. They may be used diagnostically to quantitate
CC   the expression of the polypeptide by patients and hence which subjects
CC   may be in need of restorative therapy.
XX
SQ   Sequence   288 AA;

Query Match             100.0%;  Score 1149;  DB 21;  Length 288;
Best Local Similarity   100.0%;  Pred. No. 2.6e-103;
Matches  216;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         27 glshfcsgvihvtkevkevatlscghnvsveelaqtriywqkekkmvltmmsgdmniwpe 86

Qy         61 YKNRTFDIINNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         87 yknrtfdiinnlsivilalrpsdegtyecvvlkyekdafkrehlaevtlsvkadfptps 146
```

```
Qy        121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 isdfeiptsnirriicstsggfpephlswlengeelnainttvsqdpetelyavssk.ldf 206

Qy        181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHRPDN 216
              ||||||||||||||||||||||||||||||||||||
Db        207 nmttnhsfmclikyghlrvnqtfnwnttkqehfpdn 242

RESULT   9
ID   AAU05121 standard; Protein; 288 AA.
XX
AC   AAU05121;
XX
DT   24-OCT-2001  (first entry)
XX
DE   Colorectal tumour antigen CD80.
XX
KW   Colorectal cancer; immunostimulant; cytostatic; immune response;
KW   adenocarcinoma; allogeneic tumour cell; SW620 cell; COLO 205 cell;
KW   SW403 cell; colon; breast; lung; prostate; cancer; vaccine;
KW   tumour antigen CD80.
XX
OS   Homo sapiens.
XX
PN   WO200154716-A2.
XX
PD   02-AUG-2001.
XX
PF   26-JAN-2001;   2001WO-US02731.
XX
PR   27-JAN-2000;   2000US-0178498.
PR   28-FEB-2000;   2000US-0185335.
XX
PA   (KIMM-) KIMMEL CANCER CENT SIDNEY.
PA   (IMMU-) IMMUNE RESPONSE CORP.
XX
PI   Sobol RE, Shawler DL, Bartholomew RM, Carlo DJ, Gold DP;
XX
DR   WPI; 2001-502616/55.
DR   N-PSDB; AAS11426.
XX
PT   New composition comprising an allogeneic tumour cell, useful for
PT   stimulating an immune response in a patient having an adenocarcinoma,
PT   especially useful for treating colorectal, breast, lung or prostate
PT   cancer -
XX
PS   Example 2: Page 130-131; 131pp; English.
XX
CC   The invention relates to a composition for stimulating an immune response
CC   in a patient having an adenocarcinoma or colorectal cancer. The
CC   composition comprises an allogeneic tumour cell selected from SW620 cell,
CC   COLO 205 cell and SW403 cell, and a physiological carrier. The allogeneic
CC   cell stimulates an immune response to an autologous tumour cell in the
CC   patient. The composition is useful for stimulating an immune response in
CC   a patient having an adenocarcinoma, e.g. colon, breast, lung or prostate
CC   adenocarcinoma. The use of allogeneic tumour cells provides a generic
CC   source of antigen that can be administered to a variety of patients, in
CC   contrast to using autologous tumour cells, which must be isolated from
CC   each individual patient. The allogeneic cells are suitable as a cancer
CC   vaccine and can stimulate an immune response against autologous tumour
CC   cells of a cancer patient. The present sequence represents the amino acid
CC   sequence of colorectal tumour antigen CD80 used in the method of the
CC   invention.
XX
SQ   Sequence   288 AA;

Query Match             100.0%;  Score 1149;  DB 22;  Length 288;
Best Local Similarity   100.0%;  Pred. No. 2.6e-103;
Matches  216;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy    1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   27 glshfcsgvihvtkevkevatlscghnvsveelaqtriywqkekkmvltmmsgdmniwpe 86

Qy   61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   87 yknrtifditnnlsivilalrpsdegtyecvvlkyekdafkrehlaevtlsvkadfptps 146

Qy  121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  147 isdfeiptsnirriicstsggfpephlswlengeelnainttvsqdpetelyavsskldf 206

Qy  181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
        ||||||||||||||||||||||||||||||||||||
Db  207 nmttnhsfmclikyghlrvnqtfnwnttkqehfpdn 242
```

```
RESULT 10
AAB19959
ID   AAB19959 standard; Protein; 288 AA.
XX
AC   AAB19959;
XX
DT   19-MAR-2001 (first entry)
XX
DE   Human B lymphocyte antigen B7.
XX
KW   Human; B7; B lymphocyte; antigen; T cell costimulatory molecule;
KW   CD28; CTLA4; tumour; melanoma; neuroblastoma; leukaemia; carcinoma;
KW   metastasis; antitumour; therapy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FH
FT   Peptide         1..34
FT                   /label= Signal_peptide
FT   Protein         35..288
FT                   /label= Mature_protein
FT   Protein         35..242
FT                   /note= "extracellular domain"
FT   Domain          243..269
FT                   /note= "transmembrane domain"
FT   Domain          270..288
FT                   /note= "intracellular domain"
FT   Domain          35..138
FT                   /note= "immunoglobulin V-set domain"
FT   Domain          139..236
FT                   /note= "immunoglobulin C-set domain"
FT   Modified-site   53..55
FT                   /note= "Asn is N-glycosylated"
FT   Modified-site   89..91
FT                   /note= "Asn is N-glycosylated"
FT   Modified-site   98..100
FT                   /note= "Asn is N-glycosylated"
FT   Modified-site   186..188
FT                   /note= "Asn is N-glycosylated"
FT   Modified-site   207..209
FT                   /note= "Asn is N-glycosylated"
FT   Modified-site   211..213
FT                   /note= "Asn is N-glycosylated"
FT   Modified-site   226..228
FT                   /note= "Asn is N-glycosylated"
FT   Modified-site   232..234
FT                   /note= "Asn is N-glycosylated"
XX
PN   US6149905-A.
XX
PD   21-NOV-2000.
XX
PF   23-SEP-1998; 98US-0159135.
XX
PR   03-NOV-1993; 93US-0147772.
XX
PA   (GEMY ) GENETICS INST INC.
PA   (DAND ) DANA FARBER CANCER INST INC.
PA   (HARD ) HARVARD COLLEGE.
XX
PI   Baskar S, Glimcher LH, Freeman GJ, Ostrand-Rosenberg S;
PI   Nadler LM;
XX
DR   WPI; 2001-079388/09.
DR   N-PSDB; AAA89224.
XX
PT   Modifying tumour cell for treating tumors, reducing metastatic spread,
PT   inhibiting recurrence of tumor and increasing immunogenicity, involves
PT   transfecting tumour cells with a nucleic acid encoding B7 molecule -
XX
PS   Claim 4; Column 31-34; 24pp; English.
XX
CC   The present sequence is that of human lymphocyte antigen B7, a T
CC   cell costimulatory molecule that binds to CD28 and CTLA4. Tumour
CC   cells modified to express a T cell costimulatory molecule,
CC   especially B7, are disclosed. The tumour cells are modified by
CC   transfection with a nucleic acid encoding the T cell costimulatory
CC   molecule, by using an agent which induces or increases expression
CC   of the T cell costimulatory molecule on the tumour cell surface, or
CC   by coupling the T cell costimulatory molecule to the tumour cell
CC   surface. Tumour cells further modified to express major
CC   histocompatibility complex (MHC) class I and/or class II molecules,
CC   or in which expression of an MHC associated protein, the invariant
CC   chain, is inhibited are also disclosed. The modified tumour cells
CC   are used to treat a patient with a tumour, preventing or inhibiting
CC   metastatic spread or tumour recurrence. The tumour may be a
CC   melanoma, a neuroblastoma, a leukaemia or a carcinoma. A method for
CC   specifically inducing a CD4+ T cell response against a tumour, and a
CC   method for treating a tumour by modification of tumour cells in vivo
CC   are also disclosed. The treatment methods increase the immunogenicity
CC   of the tumour cell in vivo. The antitumour T cell-mediated immune
CC   response is effective both against the modified tumour cells and the
CC   unmodified tumour cells from which the modified cells were derived.
CC   Thus, the effector phase of the antitumour response induced by the
CC   modified tumour cells is not dependent upon expression of a
CC   costimulatory molecule on the tumour cells.
XX
SQ   Sequence   288 AA;
```

```
Query Match             100.0%;  Score 1149;  DB 22;  Length 288;
Best Local Similarity   100.0%;
                                 Pred. No. 2.6e-103;
Matches  216;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   27 glshfcsgvihvtkevkevatlscghnvsveelaqtriywqkekkmvltmmsgdmniwpe 86

Qy   61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   87 yknrtifditnnlsivilalrpsdegtyecvvlkyekdafkrehlaevtlsvkadfptps 146

Qy  121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  147 isdfeiptsnirriicstsggfpephlswlengeelnainttvsqdpetelyavsskldf 206

Qy  181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
        ||||||||||||||||||||||||||||||||||||
Db  207 nmttnhsfmclikyghlrvnqtfnwnttkqehfpdn 242
```

```
RESULT 11
AAW41415
ID   AAW41415 standard; Protein; 473 AA.
XX
AC   AAW41415;
XX
DT   02-JUN-1998 (first entry)
XX
```

DE Human B7.1-murine A5B7 F(ab')2 fusion protein.
XX
KW Anti-CEA antibody; carcinoembryonic antigen; 806.077 Ab; cancer therapy;
KW cancer diagnosis; complementarity determining region.
XX
OS Chimeric - Homo sapiens.
OS Chimeric - Mus sp.
XX
PN WO9742329-A1.
XX
PD 13-NOV-1997.
XX
PF 29-APR-1997; 97WO-GB01165.
XX
PR 14-FEB-1997; 97GB-0003103.
PR 04-MAY-1996; 96GB-0009405.
XX
PA (ZENE) ZENECA LTD.
XX
PI Copley CG, Edge MD, Emery SC;
XX
DR WPI; 1997-558987/51.
DR N-PSDB; AAV17340.
XX
PT Anti-carcinoembryonic antigen antibody 806.077 Ab - used for
PT diagnosis and therapy of cancer
XX
PS Reference Example 3; Page 190-193; 208pp; English.
XX
CC This sequence is the human B7.1-murine A5B7 F(ab')2 fusion protein
CC (AB7), and is an example of the antibody of the invention. The antibody
CC is an anti-CEA (carcinoembryonic antigen) antibody (preferably
CC 806.077 Ab). Host cells or transgenic organisms transformed with DNA
CC encoding the antibody, are used to make the antibody or conjugate. The
CC conjugate is used in a medicament suitable for intravenous
CC administration. The conjugate can be used for cancer therapy, selectively
CC killing tumour cells. The antibody can be used for in vivo or in vitro
CC diagnosis of cancer.
XX
SQ Sequence 473 AA;

Query Match　　　　100.0%; Score 1149; DB 18; Length 473;
Best Local Similarity 100.0%; Pred. No. 5.3e-103;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy    1 GLSHFCSGVIHVTKVEKVEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   27 glshfcsgvihvtkvekvevatlscghnvsveelaqtriywqkekkmvltmmsgdmniwpe 86

Qy   61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   87 yknrtifditnnlsivilalrpsdegtyecvvlkyekdafkrehlaevtlsvkadfptps 146

Qy  121 ISDFEIPTSNIRIRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  147 isdfeiptsnirriicstsggfpephlswlengeelnainttvsqdpetelyavsskldf 206

Qy  181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
        ||||||||||||||||||||||||||||||||||||
Db  207 nmttnhsfmclikyghlrvnqtfnwnttkqehfpdn 242
```

RESULT 12
ID AAW90208 standard; Protein; 251 AA.
XX
AC AAW90208;
XX
DT 10-MAY-1999 (first entry)
XX
DE hB7.1glu-glu soluble fusion protein.
XX

DE B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2;
KW CD86; T cell activation; inhibitor; graft versus host disease;
KW transplant rejection; allograft rejection; autoimmune disease;
KW allergy; therapy; human; hB7.1glu-glu.
XX
OS Chimeric - Homo sapiens.
OS Chimeric - synthetic.
XX

Key	Location/Qualifiers
FT Peptide	1..34
FT	/note= "potential eukaryotic secretory signal
FT	peptide"
FT Domain	35..242
FT	/note= "human B7.1 (mature protein) extracellular
FT	domain"
FT Peptide	243..251
FT	/note= "Glu-Glu detection/purification tag"

XX
PN WO9858965-A2.
XX
PD 30-DEC-1998.
XX
PF 22-JUN-1998; 98WO-EP03791.
XX
PR 20-JUN-1997; 97EP-0870092.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI Bosman A, Buyse M, Lorre K, Sablon E;
XX
DR WPI; 1999-105615/09.
XX
PT New molecules which bind B7.1 and B7.2 - useful to prevent and treat
PT immune diseases including allograft rejection
XX
PS Example 3.1.2; Fig 4; 182pp; English.
XX
CC This 29 kDa soluble fusion molecule, termed hB7.1glu-glu, is composed
CC of human co-stimulatory molecule B7.1 extracellular domain fused
CC C-terminally to a synthetic Glu-Glu epitope (see AAW90197). It
CC was produced from total RNA of Epstein-Barr virus-transformed
CC human spleen cells by RT-PCR using primers MR67 and MR145 (see
CC AAX01601). The fusion protein has been produced in Sf9 Spodoptera
CC frugiperda insect cells using a baculovirus expression system.
CC The invention relates to molecules such as diabodies, trivalent and
CC tetravalent antibodies and small antigen binding peptides which can
CC cross-link, or cross-react with, B7.1 and B7.2 expressed on
CC professional antigen presenting cells leading to the inhibition of
CC antigen-specific T cell activation. Methods to produce such
CC molecules are provided. The molecules are used to treat or prevent
CC diseases of the immune system, in particular graft rejection, graft
CC versus host disease, allergy and autoimmune diseases (claimed).
XX
SQ Sequence 251 AA;

Query Match　　　　99.7%; Score 1146; DB 20; Length 251;
Best Local Similarity 99.5%; Pred. No. 4.2e-103;
Matches 215; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy    1 GLSHFCSGVIHVTKVEKVEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   27 glshfcsgvihvtkvekvevatlscghnvsveelaqtriywqkekkmvltmmsgdmniwpe 86

Qy   61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   87 yknrtifditnnlsivilalrpsdegtyecvvlkyekdafkrehlaevtlsvkadfptps 146

Qy  121 ISDFEIPTSNIRIRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  147 isdfeiptsnirriicstsggfpephlswlengeelnainttvsqdpetelyavsskldf 206

Qy  181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
        ||||||||||||||||||||||||||||||||||||
Db  181 nmttnhsfmclikyghlrvnqtfnwnttkqehfpdn 216
```

Db   207 nmttnhsfmclikyghlrvnqtfnwnttkqqhfpdn 242

RESULT 13

ID   AAW38415 standard; Protein; 475 AA.
XX
AC   AAW38415;
XX
DT   08-APR-1998 (first entry)
XX
DE   Soluble B7-1-Ig.
XX
KW   Soluble B7-1-Ig; Immunoglobulin.
KW   Screening; inhibitor; enhancer; binding; CD28; B7-1;
XX
OS   Homo sapiens.
XX
PN   EP795554-A2.
XX
PD   17-SEP-1997.
XX
PF   04-MAR-1997; 97EP-0301438.
XX
PR   02-OCT-1996; 96JP-0262085.
PR   05-MAR-1996; 96JP-0047795.
XX
PA   (TAKE) TAKEDA CHEM IND LTD.
XX
PI   Hattori M, Hida T, Kurokawa T, Nakanishi A;
XX
DR   WPI; 1997-450803/42.
DR   N-PSDB; AAT96359.
XX
PT   New xanthene derivatives useful as immunomodulators - e.g. methyl
PT   2-(carboxymethylsulphinyl)-5,7-dichloro-3,8-dihydroxy-6-
PT   methyl-9-oxo-9H-xanthene-1-carboxylate.
XX
PS   Disclosure; Fig 6 and 7; 117pp; English.
XX
CC   The present sequence was used in the development of a novel method
CC   for screening for compounds that inhibit or enhance binding of CD28
CC   to B7-1.
XX
SQ   Sequence 475 AA;

Query Match   99.6%; Score 1144; DB 18; Length 475;
Best Local Similarity   99.5%;
  Matches 215; Conservative   1; Mismatches   0; Indels   0; Gaps   0;

Qy   1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   27 glshfcsgvihvtkevkevatlscghnvsveelaqtriywqkekkmvltmmsgdmniwpe 86

Qy   61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   87 yknrtifditnnlsivilalrpsdegtyecvvlkyekdafkrehlaevtlsvkadfptps 146

Qy   121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   147 isdfeiptsnirriicstsggfpephlswlengeelnainttvsqdpetelyavsskldf 206

Qy   181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
             |||||||||||||||||||||||||||||||||||:
Db   207 nmttnhsfmclikyghlrvnqtfnwnttkqehfpdh 242

RESULT 14

ID   AAW86004 standard; Protein; 488 AA.
XX
AC   AAW86004;
XX
DT   15-MAR-1999 (first entry)
XX
DE   Human B7-1.5T4.1 protein fusion, specific for human 5T4.
XX
KW   Tumour interacting protein; cancer; gene therapy; vector;
KW   5T4 antigen; monoclonal antibody; single chain antibody;
KW   mouse; human; B7-1; co-stimulatory molecule.
XX
OS   Chimeric - Mus sp.
OS   Chimeric - Homo sapiens.
OS   Chimeric - synthetic.
XX
PN   WO9855607-A2.
XX
PD   10-DEC-1998.
XX
PF   04-JUN-1998; 98WO-GB01627.
XX
PR   04-JUL-1997; 97GB-0014230.
PR   04-JUN-1997; 97GB-0011579.
PR   20-JUN-1997; 97GB-0013150.
XX
PA   (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI   Bebbington CR, Carroll MW, Ellard FM, Kingsman SM,
PI   Myers KA;
XX
DR   WPI; 1999-059910/05.
DR   N-PSDB; AAV80292.
XX
PT   New vector encoding a tumour interacting protein for treating cancer
PT   - contains a desired nucleotide sequence and/or protein which
PT   recognises tumours, and is used as a gene delivery system to treat
PT   cancer
XX
PS   Example 5; Fig 2; 82pp; English.
XX
CC   This is the amino acid sequence of B7-1.5T4.1, a fusion protein
CC   comprising the extracellular domain (amino acids 1-215) of human
CC   co-stimulatory molecule B7-1 joined via a flexible peptide linker
CC   to an scFv (see AAW86002) derived from murine 5T4 monoclonal
CC   antibody. B7-1.5T4.1 cDNA (see AAV80292) can be inserted into vector
CC   pCI to allow expression of the fusion protein in mammalian cells.
CC   The trophoblast cell surface antigen defined by 5T4 is expressed at
CC   high levels on the cells of a wide variety of human tumours. The
CC   invention relates to a vector comprising a nucleotide sequence
CC   coding for a tumour interacting protein (TIP) and optionally a
CC   nucleotide sequence of interest (NOI) which encodes a protein of
CC   interest (POI), the vector being capable of delivering the NOI
CC   and/or POI to the tumour recognised by the TIP. Delivery can be in
CC   vivo or ex vivo. The vector is used to treat cancer, and may also
CC   used as a gene delivery system for introducing at least 1 gene
CC   encoding a TIP (preferably a tumour binding protein) into a
CC   haematopoietic cell lineage. B7-1 is expected to bind specifically
CC   to CD28 and CTLA-4 present on human T-cells.
XX
SQ   Sequence 488 AA;

Query Match   99.5%; Score 1143; DB 20; Length 488;
Best Local Similarity 100.0%;
  Matches 215; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   27 glshfcsgvihvtkevkevatlscghnvsveelaqtriywqkekkmvltmmsgdmniwpe 86

Qy   61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   87 yknrtifditnnlsivilalrpsdegtyecvvlkyekdafkrehlaevtlsvkadfptps 146

```
Qy  121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  147 isdfeiptsnirriicstsggfpephlswlengeelnainttvsqdpetelyavssskldf 206

Qy  181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPD 215
        |||||||||||||||||||||||||||||||||||
Db  207 nmttnhsfmclikyghlrvnqtfnwnttkqehfpd 241
```

RESULT 15

```
ID   AAB83836 standard; Protein; 488 AA.
XX
AC   AAB83836;
XX
DT   23-JUL-2001  (first entry)
XX
DE   Amino acid sequence of a B7-1.5T4.1 fusion protein.
XX
KW   Single chain antibody; ScFv; inflammatory disease; arthritis; cancer;
KW   hypersensitivity; autoimmune disease; central nervous system disorder;
KW   Parkinson's disease; periodontal disease; cardiopulmonary disease;
KW   cardiovascular disease; gastrointestinal disorder; infection; diabetes;
KW   Helicobacter-related disease; immune disorder.
XX
OS   Synthetic.
OS   Mus sp.
OS   Homo sapiens.
XX
PN   WO200136486-A2.
XX
PD   25-MAY-2001.
XX
PF   13-NOV-2000; 2000WO-GB04317.
XX
PR   18-NOV-1999; 99WO-GB03859.
PR   15-FEB-2000; 2000GB-0003527.
PR   02-MAR-2000; 2000GB-0005071.
XX
PA   (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI   Kingsman A, Kingsman SM, Bebbington CR, Carroll MW, Ellard FM;
PI   Myers KA;
XX
DR   WPI; 2001-343805/36.
DR   N-PSDB; AAF89730.
XX
PT   Use of single chain antibody capable of recognizing a disease
PT   associated molecule for manufacturing a medicament for preventing
PT   and/or treating a disease condition associated with disease associated
PT   molecule -
XX
PS   Claim 3; Fig 2; 118pp; English.
XX
CC   The specification describes the use of a single chain antibody (ScFv),
CC   which is capable of recognizing a disease associated molecule in the
CC   manufacture of a medicament for the prevention and treatment of a
CC   disease condition. The ScFv antibody is useful in the manufacture of
CC   a medicament, for affecting a disease in vivo, for preparing a
CC   pharmaceutical composition, for in vivo imaging and/or for adjuvant
CC   treatment of a disease. The ScFv antibody is also useful for
CC   treating inflammatory diseases including arthritis, hypersensitivity,
CC   autoimmune diseases, cancers, central nervous system disorders
CC   including Parkinson's disease, periodontal diseases, cardiopulmonary
CC   diseases, cardiovascular diseases, gastrointestinal disorders,
CC   infections, diabetes, Helicobacter-related diseases, and other immune
CC   disorders. The present sequence represents a B7-1.5T4.1 fusion protein.
CC   This comprises the N-terminus of the 5T4 ScFv is fused after amino acid
CC   215 of human B7-1.
XX
SQ   Sequence  488 AA;
```

```
Query Match     99.5%;  Score 1143;  DB 22;  Length 488;
Best Local Similarity   100.0%;  Pred. No. 2.1e-102;
Matches  215;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKNVLTMMSGDMNIWPE 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   27 glshfcsgvihvtkevkevatlscghnvsveelaqtriywqkekkmvltmmsgdmniwpe 86

Qy   61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYIEKDAFKREHLAEVTLSVKADFPTPS 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   87 yknrtifditnnlsivilalrpsdegtyecvvlkyekkdafkrehlaevtlsvkadfpts 146

Qy  121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  147 isdfeiptsnirriicstsggfpephlswlengeelnainttvsqdpetelyavssskldf 206

Qy  181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPD 215
        |||||||||||||||||||||||||||||||||||
Db  207 nmttnhsfmclikyghlrvnqtfnwnttkqehfpd 241
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Search completed: June 18, 2002, 11:44:32
Job time: 85 sec

OM protein - protein search, using sw model

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

Run on: June 18, 2002, 11:43:07 ; Search time 107.98 Seconds
                                                (without alignments)
                                                704.092 Million cell updates/sec

Title: US-09-454-651B-23
Perfect score: 1149
Sequence: 1 GLSHFCSGVIHVTKEVKEVA..........LRVNQTFNWNTTKQEHFPDN 216

Scoring table: BLOSUM62
                  Gapop 10.0 , Gapext 0.5

Searched: 352263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 3502263

Post-processing: Minimum Match 0%
Maximum DB seq length: 2000000000
Minimum DB seq length: 0
                  Maximum Match 100%
                  Listing first 45 summaries

Database :   Pending_Patents_AA_Main:*
                  1: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:*
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                  3: /cgn2_6/ptodata/2/paa/US07_COMB.pep:*
                  4: /cgn2_6/ptodata/2/paa/US080_COMB.pep:*
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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1149	100.0	216	8	US-08-459-766B-8	Sequence 8, Appli
2	1149	100.0	216	19	US-09-569-164A-8	Sequence 8, Appli
3	1149	100.0	226	1	PCT-US01-41430-21	Sequence 21, Appli
4	1149	100.0	248	1	PCT-US01-06769-12	Sequence 12, Appl
5	1149	100.0	288	1	PCT-US01-41430-15	Sequence 15, Appl
6	1149	100.0	288	3	US-07-751-306C-2	Sequence 2, Appli
7	1149	100.0	288	5	US-08-109-393A-29	Sequence 29, Appl

8	1149	100.0	288	5	US-08-147-773-6	Sequence 6, Appli
9	1149	100.0	288	6	US-08-280-757-29	Sequence 29, Appl
10	1149	100.0	288	8	US-08-435-816A-2	Sequence 2, Appli
11	1149	100.0	288	8	US-08-453-386-2	Sequence 2, Appli
12	1149	100.0	288	9	US-08-592-711-2	Sequence 2, Appli
13	1149	100.0	288	9	US-09-206-132-6	Sequence 6, Appli
14	1149	100.0	288	16	US-09-277-575-2	Sequence 2, Appli
15	1149	100.0	288	16	US-09-350-202-2	Sequence 2, Appli
16	1149	100.0	288	17	US-09-425-581-6	Sequence 6, Appli
17	1149	100.0	288	18	US-09-425-516-29	Sequence 29, Appl
18	1149	100.0	288	18	US-09-425-762-29	Sequence 29, Appl
19	1149	100.0	288	19	US-09-522-206-2	GENERAL INFORMA
20	1149	100.0	288	19	US-09-565-316A-2	Sequence 2, Appli
21	1149	100.0	288	20	US-09-620-461-5	Sequence 5, Appli
22	1149	100.0	288	20	US-09-651-200-13	Sequence 13, Appli
23	1149	100.0	288	20	US-09-667-135-34	Sequence 34, Appl
24	1149	100.0	288	21	US-09-711-022-2	Sequence 2, Appli
25	1149	100.0	288	21	US-09-716-928-2	Sequence 2, Appli
26	1149	100.0	288	21	US-09-716-928-8	Sequence 8, Appli
27	1149	100.0	288	21	US-09-772-102-14	Sequence 14, Appl
28	1149	100.0	288	22	US-09-837-867-19	Sequence 19, Appl
29	1149	100.0	288	22	US-09-837-867A-19	Sequence 19, Appl
30	1149	100.0	288	22	US-09-868-605-1	Sequence 1, Appli
31	1149	100.0	288	22	US-09-896-738-110	Sequence 110, Appl
32	1149	100.0	288	23	US-09-910-174A-5	Sequence 5, Appli
33	1149	100.0	288	23	US-09-962-969-19	Sequence 19, Appl
34	1149	100.0	288	23	US-09-966-148-2	Sequence 2, Appli
35	1149	100.0	288	23	US-10-041-319-7	Sequence 7, Appli
36	1149	100.0	288	24	US-09-910-059-131	Sequence 131, App
37	1149	100.0	473	23	US-09-468-029-51	Sequence 51, Appl
38	1146	99.7	251	18	PCT-US97-12599-3	Sequence 3, Appl
39	1143	99.5	492	16	US-09-202-346-3	Sequence 3, Appli
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45	1138	99.0	480	18	US-09-468-029-49	Sequence 49, Appl

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT   1
US-08-459-766B-8

Sequence 8, Application US/08459766B
GENERAL INFORMATION:
APPLICANT: Linsley, Peter S.
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Damle, Nitin K.
APPLICANT: Brady, William
TITLE OF INVENTION: LIGAND FOR CD28 RECEPTOR ON B CELLS AND METHODS
FILE REFERENCE: 30436.11US04
CURRENT APPLICATION NUMBER: US/08/459,766B
CURRENT FILING DATE: 1995-06-02
PRIOR APPLICATION NUMBER: 07/498,949
PRIOR APPLICATION NUMBER: 07/547,980
PRIOR FILING DATE: 1990-03-26
PRIOR FILING DATE: 1990-07-02
PRIOR APPLICATION NUMBER: 07/722,101
PRIOR FILING DATE: 1991-06-27
PRIOR APPLICATION NUMBER: 08/219,200
PRIOR FILING DATE: 1994-03-29
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 8
LENGTH: 216
TYPE: PRT
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
AUTHORS: Freeman, Gordon J.
AUTHORS: Freedman, Arnold S.
AUTHORS: Segil, Jeffrey M.

AUTHORS: Lee, Grace
AUTHORS: Whitman, James F.
AUTHORS: Nadler, Lee M.
TITLE: B7, A NEW MEMBER OF THE Ig SUPERFAMILY WITH UNIQUE
TITLE: EXPRESSION ON ACTIVATED AND NEOPLASTIC B CELLS
US-08-459-766B-8

Query Match   100.0%;   Score 1149;   DB 8;   Length 216;
Best Local Similarity 100.0%;   Pred. No. 6.4e-112;
Matches 216;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

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Db   1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60

Qy  61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
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Db  61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120

Qy 121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
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Qy 181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
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Db 181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
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RESULT 2
US-09-569-164A-8
Sequence 8, Application US/09569164A
GENERAL INFORMATION:
APPLICANT: LINSLEY, PETER S. ET AL.
TITLE OF INVENTION: LIGAND FOR CD28 RECEPTOR ON B CELLS AND METHODS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/569,164A
CURRENT FILING DATE: 2000-05-11
PRIOR APPLICATION NUMBER: 09/569,164A
PRIOR FILING DATE: 2000-05-11
PRIOR APPLICATION NUMBER: 07/547,980
PRIOR FILING DATE: 1990-07-02
PRIOR APPLICATION NUMBER: 07/722,101
PRIOR FILING DATE: 1991-06-27
PRIOR APPLICATION NUMBER: 08/219,200
PRIOR FILING DATE: 1994-03-29
PRIOR APPLICATION NUMBER: 08/459,766
PRIOR FILING DATE: 1995-06-02
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
LENGTH: 216
TYPE: PRT
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
AUTHORS: Freeman, Gordon J.
AUTHORS: Freedman, Arnold S.
AUTHORS: Segil, Jeffrey M.
AUTHORS: Lee, Grace
AUTHORS: Whitman, James F.
AUTHORS: Nadler, Lee M.
TITLE: B7, A NEW MEMBER OF THE IG SUPERFAMILY WITH UNIQUE
TITLE: EXPRESSION ON ACTIVATED AND NEOPLASTIC B CELLS
US-09-569-164A-8

Query Match   100.0%;   Score 1149;   DB 19;   Length 216;
Best Local Similarity 100.0%;   Pred. No. 6.4e-112;
Matches 216;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

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Qy   1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
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Qy  61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
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Db  61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120

Qy 121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180

Qy 181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
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RESULT 3
PCT-US01-41430-21
Sequence 21, Application PCT/US0141430
GENERAL INFORMATION:
APPLICANT: Mayo Foundation for Medical Education and Research
TITLE OF INVENTION: B7-H3 AND B7-H4, NOVEL IMMUNOREGULATORY
FILE REFERENCE: 07039-219W01
CURRENT APPLICATION NUMBER: PCT/US01/41430
CURRENT FILING DATE: 2001-07-26
PRIOR APPLICATION NUMBER: 60/220,991
PRIOR FILING DATE: 2000-07-27
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 21
LENGTH: 226
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US01-41430-21

Query Match   100.0%;   Score 1149;   DB 1;   Length 226;
Best Local Similarity 100.0%;   Pred. No. 6.8e-112;
Matches 216;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

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Qy   1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
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Db  11 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 70

Qy  61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
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Db  71 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 130

Qy 121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 131 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 190

Qy 181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
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Db 191 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 226
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RESULT 4
PCT-US01-06769-12
Sequence 12, Application PCT/US0106769
GENERAL INFORMATION:
APPLICANT: Mayo Medical Ventures
TITLE OF INVENTION: hB7-H2, A NOVEL CO-STIMULATORY MOLECULE
FILE REFERENCE: 07039-202W01

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  CURRENT APPLICATION NUMBER: PCT/US01/06769
  CURRENT FILING DATE: 2001-03-02
  PRIOR APPLICATION NUMBER: 60/186,519
  PRIOR FILING DATE: 2000-03-02
  NUMBER OF SEQ ID NOS: 13
  SOFTWARE: FastSEQ for Windows Version 4.0

  SEQ ID NO 12
  LENGTH: 248
  TYPE: PRT
  ORGANISM: Homo sapiens
PCT-US01-06769-12
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Query Match                      100.0%;  Score 1149;  DB 1;  Length 248;
Best Local Similarity   100.0%;  Pred. No. 7.8e-112;
Matches  216;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
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Qy   61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADPPTPS 120
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Db   87 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADPPTPS 146

Qy  121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206

Qy  181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
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Db  207 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242
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RESULT  5
PCT-US01-41430-15
  Sequence 15, Application PC/TUS0141430
  GENERAL INFORMATION:
    APPLICANT: Mayo Foundation for Medical Education and Research
    TITLE OF INVENTION: B7-H3 AND B7-H4, NOVEL IMMUNOREGULATORY
    TITLE OF INVENTION: MOLECULES
    FILE REFERENCE: 07039-219W01
    CURRENT APPLICATION NUMBER: PCT/US01/41430
    CURRENT FILING DATE: 2001-07-26
    PRIOR APPLICATION NUMBER: 60/220,991
    PRIOR FILING DATE: 2000-07-27
    SOFTWARE: FastSEQ for Windows Version 4.0
    NUMBER OF SEQ ID NOS: 23

  SEQ ID NO 15
    LENGTH: 288
    TYPE: PRT
    ORGANISM: Homo sapiens
PCT-US01-41430-15
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Query Match              100.0%;  Score 1149;  DB 1;  Length 288;
Best Local Similarity   100.0%;  Pred. No. 9.7e-112;
Matches  216;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86

Qy   61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADPPTPS 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   87 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADPPTPS 146

Qy  121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206

Qy  181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
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Db  207 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242
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```
RESULT  6
US-07-751-306C-2
  Sequence 2, Application US/07751306C
  GENERAL INFORMATION:
    APPLICANT: FREEMAN, GORDON J.
    APPLICANT: FREEDMAN, ARNOLD S.
    APPLICANT: NADLER, LEE M.
    TITLE OF INVENTION: DNA Encoding B7, A New Member
    TITLE OF INVENTION: Of The IgG Superfamily With Unique Expression On
    TITLE OF INVENTION: Activated And Neoplastic B Cells.
    NUMBER OF SEQUENCES: 4
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: The Dana-Farber Cancer Institute
    STREET: 44 Binney Street
    CITY: Boston
    STATE: Massachusetts
    COUNTRY: U.S.A.
    ZIP: 02115
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Diskette, 3.50 inch, 720kb storage
    COMPUTER: IBM Personal System 2; Model 30
    OPERATING SYSTEM: MS/DOS
    SOFTWARE: WordPerfect 5.0
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/07/751,306C
    FILING DATE: 19910828
    CLASSIFICATION: 435
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 07/591,300
    FILING DATE: 01-OCT-1990
  ATTORNEY/AGENT INFORMATION:
    NAME: HART, JULIA D.
    REGISTRATION NUMBER: 33132
    REFERENCE/DOCKET NUMBER: DFCI-116.1
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: (203) 255-8900
    TELEFAX: (203) 259-2846
  INFORMATION FOR SEQ ID NO: 2:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 288 amino acids
      TYPE: AMINO ACID
      TOPOLOGY: linear
    MOLECULE TYPE: protein
    DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein
    DESCRIPTION: B cell activation antigen; natural ligand
    OTHER INFORMATION: hydrophobic
  FEATURE:
    NAME/KEY: signal sequence
    LOCATION: -34 to -1
    IDENTIFICATION METHOD: amino terminal sequencing of
    IDENTIFICATION METHOD: soluble protein
  FEATURE:
    NAME/KEY: extracellular domain
    LOCATION: 1 to 208
    IDENTIFICATION METHOD: similarity with known
    IDENTIFICATION METHOD: sequence
  FEATURE:
    NAME/KEY: transmembrane domain
    LOCATION: 209 to 235
    IDENTIFICATION METHOD: similarity with known
    IDENTIFICATION METHOD: sequence
  FEATURE:
    NAME/KEY: intracellular domain
    LOCATION: 236 to 254
    IDENTIFICATION METHOD: similarity with known
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  FEATURE:
    NAME/KEY: N-linked glycosylation
    LOCATION: 19 to 21
    IDENTIFICATION METHOD: similarity with known
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Db  207 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242
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        IDENTIFICATION METHOD: sequence
FEATURE:
        NAME/KEY: N-linked glycosylation
        LOCATION: 55 to 57
        IDENTIFICATION METHOD: similarity with known
        IDENTIFICATION METHOD: sequence
FEATURE:
        NAME/KEY: N-linked glycosylation
        LOCATION: 64 to 66
        IDENTIFICATION METHOD: similarity with known
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FEATURE:
        NAME/KEY: N-linked glycosylation
        LOCATION: 152 to 154
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FEATURE:
        NAME/KEY: N-linked glycosylation
        LOCATION: 177 to 179
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FEATURE:
        NAME/KEY: N-linked glycosylation
        LOCATION: 192 to 194
        IDENTIFICATION METHOD: similarity with known
        IDENTIFICATION METHOD: sequence
FEATURE:
        NAME/KEY: N-linked glycosylation
        LOCATION: 198 to 200
        IDENTIFICATION METHOD: similarity with known
        IDENTIFICATION METHOD: sequence
FEATURE:
        NAME/KEY: Ig V-set domain
        LOCATION: 1 to 104
        IDENTIFICATION METHOD: similarity with known
        IDENTIFICATION METHOD: sequence
FEATURE:
        NAME/KEY: Ig C-set domain
        LOCATION: 105 to 202
        IDENTIFICATION METHOD: similarity with known
        IDENTIFICATION METHOD: sequence
PUBLICATION INFORMATION:
        AUTHORS: FREEMAN, GORDON J.
        AUTHORS: FREEDMAN, ARNOLD S.
        AUTHORS: SEGIL, JEFFREY M.
        AUTHORS: LEE, GRACE
        AUTHORS: WHITMAN, JAMES F.
        AUTHORS: NADLER, LEE M.
        TITLE: B7, A New Member Of The Ig Superfamily With
        TITLE: Unique Expression On Activated And Neoplastic B Cells
        JOURNAL: The Journal of Immunology
        VOLUME: 143
        ISSUE: 8
        PAGES: 2714-2722
        DATE: 15-OCT-1989

US-07-751-306C-2
RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262

Query Match             100.0%;  Score 1149;  DB 3;  Length 288;
Best Local Similarity   100.0%;  Pred. No. 9.7e-112;
Matches  216;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86

Qy   61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPPS 120
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RESULT 7
US-08-109-393A-29
Sequence 29, Application US/0810393A
GENERAL INFORMATION:
        APPLICANT: Freeman, Gordon J.
        APPLICANT: Nadler, Lee M.
        APPLICANT: Gray, Gary S.
        TITLE OF INVENTION: Novel CTLA4/CD28 Ligands and
        TITLE OF INVENTION: Uses Therefor
        NUMBER OF SEQUENCES: 31
        CORRESPONDENCE ADDRESS:
            ADDRESSEE: LAHIVE & COCKFIELD
            STREET: 60 State Street, Suite 510
            CITY: Boston
            STATE: Massachusetts
            COUNTRY: USA
            ZIP: 02109
        COMPUTER READABLE FORM:
            MEDIUM TYPE: Floppy disk
            COMPUTER: IBM PC compatible
            OPERATING SYSTEM: PC-DOS/MS-DOS
            SOFTWARE: PatentIn Release #1.0, Version #1.25
        CURRENT APPLICATION DATA:
            APPLICATION NUMBER: US/08/109,393A
            FILING DATE: 19-AUG-1993
            CLASSIFICATION: 435
        PRIOR APPLICATION DATA:
            APPLICATION NUMBER: 08/101,624
            FILING DATE: 26-JUL-1993
        ATTORNEY/AGENT INFORMATION:
            NAME: Mandragouras, Amy E.
            REGISTRATION NUMBER: 36,207
            REFERENCE/DOCKET NUMBER: RPI-004CP
        TELECOMMUNICATION INFORMATION:
            TELEPHONE: (617) 227-7400
            TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 29:
        SEQUENCE CHARACTERISTICS:
            LENGTH: 288 amino acids
            TYPE: amino acid
            TOPOLOGY: linear
        MOLECULE TYPE: protein
        DESCRIPTION: B cell activation antigen; natural ligand
        DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein
FEATURE:
        NAME/KEY: signal sequence
        LOCATION: -34 to -1
        IDENTIFICATION METHOD: amino terminal sequencing of
        IDENTIFICATION METHOD: soluble protein
        OTHER INFORMATION: hydrophobic
FEATURE:
        NAME/KEY: extracellular domain
        LOCATION: 1 to 208
        IDENTIFICATION METHOD: similarity with known
        IDENTIFICATION METHOD: sequence
FEATURE:
        NAME/KEY: transmembrane domain
        LOCATION: 209 to 235
        IDENTIFICATION METHOD: similarity with known
        IDENTIFICATION METHOD: sequence
FEATURE:

         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   87 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPPS 146

Qy  121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206

Qy  181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
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Db  207 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242
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NAME/KEY: intracellular domain
LOCATION: 236 to 254
IDENTIFICATION METHOD: similarity with known
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 19 to 21
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 55 to 57
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 64 to 66
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 152 to 154
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 173 to 175
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 192 to 194
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 177 to 179
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 198 to 200
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig C-set domain
LOCATION: 105 to 202
IDENTIFICATION METHOD: similarity with known
FEATURE:
NAME/KEY: Ig V-set domain
LOCATION: 1 to 104
IDENTIFICATION METHOD: similarity with known
FEATURE:

PUBLICATION INFORMATION:
AUTHORS: FREEMAN, GORDON J.
AUTHORS: FREEMAN, ARNOLD S.
AUTHORS: SEGIL, JEFFREY M.
AUTHORS: LEE, GRACE
AUTHORS: WHITMAN, JAMES F.
AUTHORS: NADLER, LEE M.
TITLE: B7, A New Member Of The Ig Superfamily With
TITLE: Unique Expression On Activated And Neoplastic B Cells
JOURNAL: The Journal of Immunology
VOLUME: 143
ISSUE: 8
PAGES: 2714-2722
DATE: 15-OCT-1989

US-08-109-393A-29

Query Match   100.0%;   Score 1149;   DB 5;   Length 288;
RELEVANT RESIDUES IN SEQ ID NO: 29; From -26 to 262

Best Local Similarity 100.0%; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches 216;

Qy   1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86

Qy   61 YKNRIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADPPTPS 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   87 YKNRIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADPPTPS 146

Qy 121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206

Qy 181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
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Db 207 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242

RESULT 8
US-08-147-773-6
Sequence 6, Application US/08147773
GENERAL INFORMATION:
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
APPLICANT: Gray, Gary S.
TITLE OF INVENTION: TUMOR CELLS MODIFIED TO EXPRESS B7-2 AND B7-3 WITH INCREASE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
   ADDRESSEE: LAHIVE & COCKFIELD
   STREET: 60 State Street, Suite 510
   CITY: Boston
   STATE: Massachusetts
   COUNTRY: USA
   ZIP: 02109
COMPUTER READABLE FORM:
   MEDIUM TYPE: Floppy disk
   COMPUTER: IBM PC Compatible
   OPERATING SYSTEM: PC-DOS/MS-DOS
   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
   APPLICATION NUMBER: US/08/147,773
   FILING DATE:
   CLASSIFICATION:
PRIOR APPLICATION DATA:
   APPLICATION NUMBER: 514
   APPLICATION NUMBER: 08/101,624;
   FILING DATE: 26-JUL-1993;
   APPLICATION NUMBER: 08/109,393;
   FILING DATE: 19-AUG-1993
ATTORNEY/AGENT INFORMATION:
   NAME: Mandragouras, Amy E.
   REGISTRATION NUMBER: 36,207
   REFERENCE/DOCKET NUMBER: RPI-008
TELECOMMUNICATION INFORMATION:
   TELEPHONE: (617) 227-7400
   TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 6:
   SEQUENCE CHARACTERISTICS:
   LENGTH: 288 amino acids
   TYPE: amino acid
   TOPOLOGY: linear
   MOLECULE TYPE: protein

US-08-147-773-6

Query Match   100.0%;   Score 1149;   DB 5;   Length 288;
Best Local Similarity 100.0%;   Pred. No. 9.7e-112;
Matches 216;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

Qy   1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86

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Qy   61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADPPTPS 120
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Db   87 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADPPTPS 146

Qy  121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206

Qy  181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
         ||||||||||||||||||||||||||||||||||||
Db  207 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242
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RESULT 9
US-08-280-757-29
Sequence 29, Application US/08280757

GENERAL INFORMATION:
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
APPLICANT: Gray, Gary S.
APPLICANT: Greenfield, Edward
TITLE OF INVENTION: Novel CTLA4/CD28 Ligands and
TITLE OF INVENTION: Uses Therefor
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/280,757
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/101,624; 08/109,393; 08/147,773
FILING DATE: 26-JUL-1993; 19-AUG-1993; 03-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-004CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: B cell activation antigen; natural ligand
DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein
FEATURE:
NAME/KEY: signal sequence
LOCATION: -34 to -1
IDENTIFICATION METHOD: amino terminal sequencing of
IDENTIFICATION METHOD: soluble protein
OTHER INFORMATION: hydrophobic
FEATURE:
NAME/KEY: extracellular domain
LOCATION: 1 to 208
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: transmembrane domain
LOCATION: 209 to 235

IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: intracellular domain
LOCATION: 236 to 254
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 55 to 57
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 64 to 66
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 19 to 21
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 152 to 154
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 173 to 175
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 192 to 194
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 177 to 179
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 198 to 200
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig V-set domain
LOCATION: 1 to 104
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig C-set domain
LOCATION: 105 to 202
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
PUBLICATION INFORMATION:
AUTHORS: FREEMAN, GORDON J.
AUTHORS: FREEDMAN, ARNOLD S.
AUTHORS: SEGIL, JEFFREY M.
AUTHORS: LEE, GRACE
AUTHORS: WHITMAN, JAMES F.
AUTHORS: NADLER, LEE M.
TITLE: B7, A New Member Of The Ig Superfamily With
TITLE: Unique Expression On Activated And Neoplastic B Cells
JOURNAL: The Journal of Immunology
VOLUME: 143
ISSUE: 8
PAGES: 2714-2722
DATE: 15-OCT-1989
RELEVANT RESIDUES IN SEQ ID NO: 29: From -26 to 262
US-08-280-757-29

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Qy  Query Match        100.0%;  Score 1149;  DB 6;  Length 288;
    Best Local Similarity  100.0%;  Pred. No. 9.7e-112;
    Matches 216;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy   1  GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE  60
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Db  27  GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE  86

Qy  61  YKNRTIFDITNNLSIVILALRPSDEGTYECVLKYEKDAFKREHLAEVTLSVKADFPTPS  120
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Db  87  YKNRTIFDITNNLSIVILALRPSDEGTYECVLKYEKDAFKREHLAEVTLSVKADFPTPS  146

Qy 121  ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF  180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 147  ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF  206

Qy 181  NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN  216
        ||||||||||||||||||||||||||||||||||||
Db 207  NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN  242
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RESULT 10
US-08-435-816A-2
Sequence 2, Application US/08435816A
GENERAL INFORMATION:
   APPLICANT: June, Carl H.
   APPLICANT: Thompson, Craig B.
   APPLICANT: Nabel, Gary J.
   APPLICANT: Gray, Gary S.
   APPLICANT: Rennert, Paul D.
   TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells
   NUMBER OF SEQUENCES: 14
   CORRESPONDENCE ADDRESS:
      ADDRESSEE: LAHIVE & COCKFIELD
      STREET: 60 State Street, Suite 510
      CITY: Boston
      STATE: Massachusetts
      COUNTRY: USA
      ZIP: 02109
   COMPUTER READABLE FORM:
      MEDIUM TYPE: Floppy disk
      COMPUTER: IBM PC compatible
      OPERATING SYSTEM: PC-DOS/MS-DOS
      SOFTWARE: PatentIn Release #1.0, Version #1.25
   CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/08/435,816A
      FILING DATE: May 4, 1995
      CLASSIFICATION: 435
   PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 08/403,253
      FILING DATE: 10 MARCH 1995
      APPLICATION NUMBER: US 08/253,964
      FILING DATE: 3 JUNE 1994
      APPLICATION NUMBER: US 08/073,223
      FILING DATE: 4 JUNE 1993
      APPLICATION NUMBER: US 08/200,947
      FILING DATE: 23 FEB 1994
      APPLICATION NUMBER: US 07/864,805
      FILING DATE: 7 APR 1992
      APPLICATION NUMBER: US 08/247,505
      FILING DATE: 23 MAY 1994
      APPLICATION NUMBER: US 07/864,866
      FILING DATE: 7 APR 1992
      APPLICATION NUMBER: US 08/218,155
      FILING DATE: 25 MAR 1994
      APPLICATION NUMBER: US 07/864,807
      FILING DATE: 7 APR 1992
      APPLICATION NUMBER: US 07/902,467
      FILING DATE: 16 JUNE 1992
      APPLICATION NUMBER: US 07/275,433
      FILING DATE: 23 NOV 1988

ATTORNEY/AGENT INFORMATION:
   NAME: Mandragouras, Amy E.
   REGISTRATION NUMBER: 36,207
   REFERENCE/DOCKET NUMBER: RPI-002CP3
   TELECOMMUNICATION INFORMATION:
      TELEPHONE: (617) 227-7400
      TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
   SEQUENCE CHARACTERISTICS:
      LENGTH: 288 amino acids
      TYPE: amino acid
      TOPOLOGY: linear
   MOLECULE TYPE: protein
      DESCRIPTION: B cell activation antigen; natural ligand
      DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein
   FEATURE:
      NAME/KEY: signal sequence
      LOCATION: -34 to -1
      IDENTIFICATION METHOD: amino terminal sequencing of
      OTHER INFORMATION: hydrophobic
   FEATURE:
      NAME/KEY: extracellular domain
      LOCATION: 1 to 208
      IDENTIFICATION METHOD: similarity with known
      IDENTIFICATION METHOD: sequence
   FEATURE:
      NAME/KEY: transmembrane domain
      LOCATION: 209 to 235
      IDENTIFICATION METHOD: similarity with known
      IDENTIFICATION METHOD: sequence
   FEATURE:
      NAME/KEY: intracellular domain
      LOCATION: 236 to 254
      IDENTIFICATION METHOD: similarity with known
      IDENTIFICATION METHOD: sequence
   FEATURE:
      NAME/KEY: N-linked glycosylation
      LOCATION: 19 to 21
      IDENTIFICATION METHOD: similarity with known
      IDENTIFICATION METHOD: sequence
   FEATURE:
      NAME/KEY: N-linked glycosylation
      LOCATION: 55 to 57
      IDENTIFICATION METHOD: similarity with known
      IDENTIFICATION METHOD: sequence
   FEATURE:
      NAME/KEY: N-linked glycosylation
      LOCATION: 64 to 66
      IDENTIFICATION METHOD: similarity with known
      IDENTIFICATION METHOD: sequence
   FEATURE:
      NAME/KEY: N-linked glycosylation
      LOCATION: 152 to 154
      IDENTIFICATION METHOD: similarity with known
      IDENTIFICATION METHOD: sequence
   FEATURE:
      NAME/KEY: N-linked glycosylation
      LOCATION: 173 to 175
      IDENTIFICATION METHOD: similarity with known
      IDENTIFICATION METHOD: sequence
   FEATURE:
      NAME/KEY: N-linked glycosylation
      LOCATION: 177 to 179
      IDENTIFICATION METHOD: similarity with known
      IDENTIFICATION METHOD: sequence
   FEATURE:
      NAME/KEY: N-linked glycosylation
      LOCATION: 192 to 194
      IDENTIFICATION METHOD: similarity with known
      IDENTIFICATION METHOD: sequence
   FEATURE:
      NAME/KEY: N-linked glycosylation

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RESULT 11
US-08-453-386-2
Sequence 2, Application US/08453386
  GENERAL INFORMATION:
    APPLICANT: FREEMAN, GORDON J.
    APPLICANT: FREEMAN, ARNOLD S.
    APPLICANT: NADLER, LEE M.
    TITLE OF INVENTION: DNA Encoding B7, A New Member
    TITLE OF INVENTION: Of The IgG Superfamily With Unique Expression On
    TITLE OF INVENTION: Activated And Neoplastic B Cells.
    NUMBER OF SEQUENCES: 4
    CORRESPONDENCE ADDRESS:
      ADDRESSEE: The Dana-Farber Cancer Institute
      STREET: 44 Binney Street
      CITY: Boston
      STATE: Massachusetts
      COUNTRY: U.S.A.
      ZIP: 02115
    COMPUTER READABLE FORM:
      MEDIUM TYPE: Diskette, 3.50 inch, 720kb storage
      COMPUTER: IBM Personal System 2; Model 30
      OPERATING SYSTEM: MS/DOS
      SOFTWARE: WordPerfect 5.0
    CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/08/453,386
      FILING DATE: 30-MAY-1995
      CLASSIFICATION: 435
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 07/751,306
      FILING DATE: 28-AUG-1991
      APPLICATION NUMBER: US 07/591,300
      FILING DATE: 01-OCT-1990
    ATTORNEY/AGENT INFORMATION:
      NAME: HART, JULIA D.
      REGISTRATION NUMBER: 33132
      REFERENCE/DOCKET NUMBER: DFCI-116.1
    TELECOMMUNICATION INFORMATION:
      TELEPHONE: (203) 255-8900
      TELEFAX: (203) 259-2846
  INFORMATION FOR SEQ ID NO: 2:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 288 amino acids
      TYPE: amino acid
      TOPOLOGY: linear
    MOLECULE TYPE: protein
      DESCRIPTION: B cell activation antigen; natural ligand
      DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein
    FEATURE:
      NAME/KEY: signal sequence
      LOCATION: -34 to -1
      IDENTIFICATION METHOD: amino terminal sequencing of
      OTHER INFORMATION: hydrophobic
    FEATURE:
      NAME/KEY: extracellular domain
      LOCATION: 1 to 208
      IDENTIFICATION METHOD: similarity with known
      IDENTIFICATION METHOD: soluble protein
      IDENTIFICATION METHOD: sequence
    FEATURE:
      NAME/KEY: transmembrane domain
      LOCATION: 209 to 235
      IDENTIFICATION METHOD: similarity with known
      IDENTIFICATION METHOD: sequence
    FEATURE:
      NAME/KEY: intracellular domain
      LOCATION: 236 to 254
      IDENTIFICATION METHOD: similarity with known
      IDENTIFICATION METHOD: sequence
    FEATURE:
      NAME/KEY: N-linked glycosylation
      LOCATION: 19 to 21
      IDENTIFICATION METHOD: similarity with known
      IDENTIFICATION METHOD: sequence
    FEATURE:
      NAME/KEY: N-linked glycosylation
      LOCATION: 55 to 57
      IDENTIFICATION METHOD: similarity with known
      IDENTIFICATION METHOD: sequence
    FEATURE:
      NAME/KEY: N-linked glycosylation
      LOCATION: 64 to 66
      IDENTIFICATION METHOD: similarity with known
      IDENTIFICATION METHOD: sequence
    FEATURE:
      NAME/KEY: N-linked glycosylation
      LOCATION: 152 to 154
      IDENTIFICATION METHOD: similarity with known
      IDENTIFICATION METHOD: sequence
    FEATURE:
      NAME/KEY: N-linked glycosylation
      LOCATION: 173 to 175
      IDENTIFICATION METHOD: similarity with known
      IDENTIFICATION METHOD: sequence
    FEATURE:
      NAME/KEY: N-linked glycosylation
      LOCATION: 198 to 200
      IDENTIFICATION METHOD: similarity with known
      IDENTIFICATION METHOD:
    FEATURE:
      NAME/KEY: Ig V-set domain
      LOCATION: 1 to 104
      IDENTIFICATION METHOD: similarity with known
      IDENTIFICATION METHOD: sequence
    FEATURE:
      NAME/KEY: Ig C-set domain
      LOCATION: 105 to 202
      IDENTIFICATION METHOD: similarity with known
      IDENTIFICATION METHOD: sequence
    PUBLICATION INFORMATION:
      AUTHORS: FREEMAN, GORDON J.
      AUTHORS: FREEMAN, ARNOLD S.
      AUTHORS: SEGIL, JEFFREY M.
      AUTHORS: LEE, GRACE
      AUTHORS: WHITMAN, JAMES F.
      AUTHORS: NADLER, LEE M.
      TITLE: B7, A New Member Of The Ig Superfamily With
      TITLE: Unique Expression On Activated And Neoplastic B Cells
      JOURNAL: The Journal of Immunology
      VOLUME: 143
      ISSUE: 8
      PAGES: 2714-2722
      DATE: 15-OCT-1989
      RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262
US-08-435-816A-2

Query Match             100.0%;  Score 1149;  DB 8;  Length 288;
Best Local Similarity   100.0%;  Pred. No. 9.7e-112;
Matches  216;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86

Qy   61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADPPTPS 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   87 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADPPTPS 146

Qy  121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
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Db  147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206

Qy  181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
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Db  207 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242
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Left column

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;      NAME/KEY:               N-linked glycosylation
;      LOCATION:               177 to 179
;      IDENTIFICATION METHOD:  similarity with known
;    FEATURE:
;      NAME/KEY:               N-linked glycosylation
;      LOCATION:               192 to 194
;      IDENTIFICATION METHOD:  similarity with known
;    FEATURE:
;      NAME/KEY:               N-linked glycosylation
;      LOCATION:               198 to 200
;      IDENTIFICATION METHOD:  similarity with known
;    FEATURE:
;      NAME/KEY:               Ig C-set domain
;      LOCATION:               105 to 202
;      IDENTIFICATION METHOD:  similarity with known
;    FEATURE:
;      NAME/KEY:               Ig V-set domain
;      LOCATION:               1 to 104
;      IDENTIFICATION METHOD:  similarity with known
;    PUBLICATION INFORMATION:
;      AUTHORS:   FREEMAN, GORDON J.
;      AUTHORS:   FREEDMAN, ARNOLD S.
;      AUTHORS:   SEGIL, JEFFREY M.
;      AUTHORS:   LEE, GRACE
;      WHITMAN,   JAMES F.
;      AUTHORS:   NADLER, LEE M.
;      TITLE:     B7, A New Member Of The Ig Superfamily With
;      TITLE:     Unique Expression On Activated And Neoplastic B Cells
;      JOURNAL:   The Journal of Immunology
;      VOLUME:    143
;      ISSUE:     8
;      PAGES:     2714-2722
;      DATE:      15-OCT-1989
;      RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262

US-08-453-386-2

Query Match           100.0%;   Score 1149;  DB 8;   Length 288;
Best Local Similarity 100.0%;   Pred. No. 9.7e-112;
Matches 216;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86

Qy   61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
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Db   87 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 146

Qy  121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206

Qy  181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
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Db  207 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242

RESULT 12
US-08-453-386A-2
;  Sequence 2, Application US/0845336A
;  GENERAL INFORMATION:
;    APPLICANT:  FREEMAN, Gordon J.
;    APPLICANT:  FREEDMAN, Arnold S.
;    APPLICANT:  NADLER, Lee M.
;    TITLE OF INVENTION:  DNA Encoding B7, A New Member Of The IGG Superfamily
;    TITLE OF INVENTION:  With Unique Expression On Activated And Neoplastic B
;    TITLE OF INVENTION:  Cells
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Right column

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;    FILE REFERENCE:             RPI-014CNDV
;    CURRENT APPLICATION NUMBER: US/08/453,386A
;    CURRENT FILING DATE:        1995-05-30
;    PRIOR APPLICATION NUMBER:   08/153,262
;    PRIOR FILING DATE:          1993-11-15
;    PRIOR APPLICATION NUMBER:   07/751,306
;    PRIOR FILING DATE:          1991-08-28
;    PRIOR APPLICATION NUMBER:   07/591,300
;    PRIOR FILING DATE:          1990-01-10
;    NUMBER OF SEQ ID NOS:       7
;    SOFTWARE:                   Patentin Ver. 2.0

SEQ ID NO 2
;    LENGTH:   288
;    TYPE:     PRT
;    ORGANISM: Artificial Sequence
;    FEATURE:
;      NAME/KEY:  PEPTIDE
;      LOCATION:  (35)
;      NAME/KEY:  DOMAIN
;      LOCATION:  (1)..(208)
;      OTHER INFORMATION: Extracellular
;      NAME/KEY:  TRANSMEM
;      LOCATION:  (209)..(235)
;      NAME/KEY:  DOMAIN
;      LOCATION:  (236)..(254)
;      OTHER INFORMATION: Intracellular
;      OTHER INFORMATION: N-linked glycosylation at position 19 to 21
;      OTHER INFORMATION: N-linked glycosylation at position 55 to 57
;      OTHER INFORMATION: N-linked glycosylation at position 64 to 66
;      OTHER INFORMATION: N-linked glycosylation at position 152 to 154
;      OTHER INFORMATION: N-linked glycosylation at position 173 to 175
;      OTHER INFORMATION: N-linked glycosylation at position 177 to 179
;      OTHER INFORMATION: N-linked glycosylation at position 192 to 194
;      OTHER INFORMATION: N-linked glycosylation at position 198 to 200
;      NAME/KEY:  DOMAIN
;      LOCATION:  (105)..(202)
;      OTHER INFORMATION: Ig C-set
;      NAME/KEY:  DOMAIN
;      LOCATION:  (1)..(104)
;      OTHER INFORMATION: Ig V-set
;    PUBLICATION INFORMATION:
;      OTHER INFORMATION: Description of Artificial Sequence: Primer
;      OTHER INFORMATION: Signal sequence from positions -34 through -1
;      JOURNAL:  J. Immunol.
;      VOLUME:   143
;      ISSUE:    8
;      PAGES:    2714-2722
;      DATE:     15-OCT-1989

US-08-453-386A-2

Query Match           100.0%;   Score 1149;  DB 8;   Length 288;
Best Local Similarity 100.0%;   Pred. No. 9.7e-112;
Matches 216;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86

Qy   61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   87 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 146

Qy  121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206

Qy  181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
         ||||||||||||||||||||||||||||||||||||
Db  207 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242

RESULT 13
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US-08-592-711-2
Sequence 2, Application US/08592711
GENERAL INFORMATION:
   APPLICANT: June, Carl H.
   APPLICANT: Thompson, Craig B.
   APPLICANT: Nabel, Gary J.
   APPLICANT: Gray, Gary S.
   APPLICANT: Rennert, Paul D.
   TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells
   NUMBER OF SEQUENCES: 14
   CORRESPONDENCE ADDRESS:
      ADDRESSEE: LAHIVE & COCKFIELD
      STREET: 60 State Street
      CITY: Boston
      STATE: Massachusetts
      COUNTRY: USA
      ZIP: 02109
   COMPUTER READABLE FORM:
      MEDIUM TYPE: Floppy disk
      COMPUTER: IBM PC Compatible
      OPERATING SYSTEM: PC-DOS/MS-DOS
      SOFTWARE: PatentIn Release #1.0, Version #1.25
   CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/08/592,711
      FILING DATE: 26-JAN-1996
   PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 08/435,816
      FILING DATE: 4-MAY-1995
      APPLICATION NUMBER: US 08/403,253
      FILING DATE: 10-MARCH-1995
      APPLICATION NUMBER: US 08/253,964
      FILING DATE: 3-JUNE-1994
      APPLICATION NUMBER: US 08/073,223
      FILING DATE: 4-JUNE-1993
      APPLICATION NUMBER: US 08/200,947
      FILING DATE: 23-FEB-1994
      APPLICATION NUMBER: US 07/864,805
      FILING DATE: 7-APR-1992
      APPLICATION NUMBER: US 08/247,505
      FILING DATE: 23-MAY-1994
      APPLICATION NUMBER: US 07/864,866
      FILING DATE: 7-APR-1992
      APPLICATION NUMBER: US 08/218,155
      FILING DATE: 25-MAR-1994
      APPLICATION NUMBER: US 07/864,807
      FILING DATE: 7-APR-1992
      APPLICATION NUMBER: US 07/902,467
      FILING DATE: 16-JUNE-1992
      APPLICATION NUMBER: US 07/275,433
      FILING DATE: 23-NOV-1988
   ATTORNEY/AGENT INFORMATION:
      NAME: Mandragouras, Amy E.
      REGISTRATION NUMBER: 36,207
      REFERENCE/DOCKET NUMBER: RPI-002CP4
   TELECOMMUNICATION INFORMATION:
      TELEPHONE: (617) 227-7400
      TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
   SEQUENCE CHARACTERISTICS:
      LENGTH: 288 amino acids
      TYPE: amino acid
      TOPOLOGY: linear
   MOLECULE TYPE: protein
   DESCRIPTION: B cell activation antigen; natural ligand
   DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein
   FEATURE:
      NAME/KEY: signal sequence
      LOCATION: -34 to -1
      IDENTIFICATION METHOD: amino terminal sequencing of
      IDENTIFICATION METHOD: soluble protein
   OTHER INFORMATION: hydrophobic
   FEATURE:
      NAME/KEY: extracellular domain

LOCATION: 1 to 208
      IDENTIFICATION METHOD: similarity with known
      IDENTIFICATION METHOD: sequence
   FEATURE:
      NAME/KEY: transmembrane domain
      LOCATION: 209 to 235
      IDENTIFICATION METHOD: similarity with known
      IDENTIFICATION METHOD: sequence
   FEATURE:
      NAME/KEY: intracellular domain
      LOCATION: 236 to 254
      IDENTIFICATION METHOD: similarity with known
      IDENTIFICATION METHOD: sequence
   FEATURE:
      NAME/KEY: N-linked glycosylation
      LOCATION: 19 to 21
      IDENTIFICATION METHOD: similarity with known
      IDENTIFICATION METHOD: sequence
   FEATURE:
      NAME/KEY: N-linked glycosylation
      LOCATION: 55 to 57
      IDENTIFICATION METHOD: similarity with known
      IDENTIFICATION METHOD: sequence
   FEATURE:
      NAME/KEY: N-linked glycosylation
      LOCATION: 64 to 66
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      IDENTIFICATION METHOD: sequence
   FEATURE:
      NAME/KEY: N-linked glycosylation
      LOCATION: 152 to 154
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      IDENTIFICATION METHOD: sequence
   FEATURE:
      NAME/KEY: N-linked glycosylation
      LOCATION: 173 to 175
      IDENTIFICATION METHOD: similarity with known
      IDENTIFICATION METHOD: sequence
   FEATURE:
      NAME/KEY: N-linked glycosylation
      LOCATION: 177 to 179
      IDENTIFICATION METHOD: similarity with known
      IDENTIFICATION METHOD: sequence
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      NAME/KEY: N-linked glycosylation
      LOCATION: 192 to 194
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      IDENTIFICATION METHOD: sequence
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      LOCATION: 198 to 200
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      IDENTIFICATION METHOD: sequence
   FEATURE:
      NAME/KEY: Ig V-set domain
      LOCATION: 1 to 104
      IDENTIFICATION METHOD: similarity with known
      IDENTIFICATION METHOD: sequence
   FEATURE:
      NAME/KEY: Ig C-set domain
      LOCATION: 105 to 202
      IDENTIFICATION METHOD: similarity with known
      IDENTIFICATION METHOD: sequence
   PUBLICATION INFORMATION:
      AUTHORS: FREEMAN, GORDON J.
      AUTHORS: FREEDMAN, ARNOLD S.
      AUTHORS: SEGIL, JEFFREY M.
      AUTHORS: LEE, GRACE
      AUTHORS: WHITMAN, JAMES F.
      AUTHORS: NADLER, LEE M.
      TITLE: B7, A New Member Of The Ig Superfamily With
      TITLE: Unique Expression On Activated And Neoplastic B Cells
      JOURNAL: The Journal of Immunology

Left column

; VOLUME: 143
; ISSUE: 8
; PAGES: 2714-2722
; DATE: 15-OCT-1989
; US-08-592-711-2
; RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262

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Query Match            100.0%;   Score 1149;   DB 9;   Length 288;
Best Local Similarity  100.0%;   Pred. No. 9.7e-112;
Matches 216;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

Qy    1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86

Qy   61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPPPS 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   87 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPPPS 146

Qy  121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206

Qy  181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
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Db  207 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242
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RESULT 14
US-09-206-132-6
Sequence 6, Application US/09206132
GENERAL INFORMATION:
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
APPLICANT: Gray, Gary S.
TITLE OF INVENTION: TUMOR CELLS MODIFIED TO EXPRESS B7-2 AND B7-3
TITLE OF INVENTION: WITH INCREASED IMMUNOGENICITY AND USES THEREFOR
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/206,132
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/456,104
FILING DATE:
APPLICATION NUMBER: 08/101,624
FILING DATE: 26-JUL-1993
APPLICATION NUMBER: 08/109,393
FILING DATE: 19-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid

Right column

; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-206-132-6

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Query Match            100.0%;   Score 1149;   DB 16;   Length 288;
Best Local Similarity  100.0%;   Pred. No. 9.7e-112;
Matches 216;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

Qy    1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
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Db   27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86

Qy   61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPPPS 120
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Db   87 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPPPS 146

Qy  121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
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Db  147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206

Qy  181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
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Db  207 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242
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RESULT 15
US-09-277-575-2
Sequence 2, Application US/09277575
GENERAL INFORMATION:
APPLICANT: Newell, Martha K.
TITLE OF INVENTION: METHODS AND PRODUCTS RELATED TO
TITLE OF INVENTION: METABOLIC INTERACTIONS IN DISEASE
FILE REFERENCE: V0139/7028/HK
CURRENT APPLICATION NUMBER: US/09/277,575
CURRENT FILING DATE: 1999-03-26
EARLIER APPLICATION NUMBER: U.S. 60/277,575
EARLIER FILING DATE: 1999-03-26
EARLIER APPLICATION NUMBER: U.S. 60/082,250
EARLIER FILING DATE: 1998-04-17
EARLIER APPLICATION NUMBER: U.S. 60/094,519
EARLIER FILING DATE: 1998-07-29
EARLIER APPLICATION NUMBER: U.S. 60/101,580
EARLIER FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 288
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-277-575-2

OM protein - protein search, using sw model

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

Run on: June 18, 2002, 11:43:07 ; Search time 13.09 Seconds
                                           (without alignments)
                                           403.050 Million cell updates/sec

Title: US-09-454-651B-23
Perfect score: 1149
Sequence: 1 GLSHFCSGVIHVTKEVKEVA.............LRVNQTFNWNTTKQEHFPDN 216

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5
Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_AA:*
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                 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	1149	100.0	288	2	US-08-147-772-2	Sequence 2, Appli
2	1149	100.0	288	2	US-08-456-104-6	Sequence 6, Appli
3	1149	100.0	288	2	US-08-101-624-23	Sequence 23, Appli
4	1149	100.0	288	2	US-08-751-767A-6	Sequence 6, Appli
5	1149	100.0	288	3	US-08-153-262-2	Sequence 2, Appli
6	1149	100.0	288	4	US-08-479-744A-29	Sequence 29, Appli
7	1149	100.0	288	4	US-08-280-757B-29	Sequence 29, Appli
8	1149	100.0	288	4	US-09-159-135-2	Sequence 2, Appli
9	1149	100.0	288	4	US-08-205-697A-19	Sequence 19, Appli
10	1149	100.0	288	4	US-08-702-525-19	Sequence 19, Appli
11	1149	100.0	288	4	US-09-450-798-2	Sequence 2, Appli
12	1149	100.0	288	5	US-08-403-253A-2	Sequence 2, Appli
13	1149	100.0	288	5	PCT-US95-02576-19	Sequence 19, Appl
14	1149	100.0	473	4	US-09-171-945-131	Sequence 131, App
15	1102	95.9	208	3	US-09-460-384-36	Sequence 36, Appl
16	1050	91.4	208	3	US-08-630-172-15	Sequence 15, Appl
17	1050	91.4	208	4	US-09-375-419-15	Sequence 15, Appl
18	561	48.8	306	4	US-08-205-697A-17	Sequence 17, Appl
19	561	48.8	306	4	US-08-702-525-17	Sequence 17, Appl
20	561	48.8	306	5	PCT-US95-02576-17	Sequence 17, Appl
21	561	48.8	320	4	US-08-205-697A-2	Sequence 2, Appli
22	561	48.8	320	4	US-08-702-525-2	Sequence 2, Appli
23	561	48.8	320	5	PCT-US95-02576-2	Sequence 2, Appli
24	561	48.8	306	4	US-08-147-772-4	Sequence 4, Appli
25	558	48.6	306	2	US-08-456-104-8	Sequence 8, Appli
26	558	48.6	306	2	US-08-101-624-25	Sequence 25, Appli
27	558	48.6	306	3	US-08-153-262-4	Sequence 4, Appli
28	558	48.6	306	3	US-08-479-744A-31	Sequence 31, Appl
29	558	48.6	306	4	US-08-280-757B-31	Sequence 31, Appl
30	558	48.6	306	4	US-09-159-135-4	Sequence 4, Appli
31	558	48.6	306	4	US-09-450-798-4	Sequence 4, Appli
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33	311	27.1	200	4	US-08-702-525-9	Sequence 9, Appli
34	311	27.1	200	5	PCT-US95-02576-9	Sequence 9, Appli
35	311	27.1	214	4	US-08-205-697A-11	Sequence 11, Appli
36	311	27.1	214	4	US-08-702-525-11	Sequence 11, Appli
37	311	27.1	214	5	PCT-US95-02576-11	Sequence 11, Appli
38	250.5	21.8	212	5	US-08-702-525-63	Sequence 63, Appl
39	250.5	21.8	212	5	PCT-US95-02576-63	Sequence 63, Appl
40	250.5	21.8	226	4	US-08-702-525-65	Sequence 65, Appl
41	250.5	21.8	226	5	PCT-US95-02576-65	Sequence 65, Appl
42	182	15.8	323	5	PCT-US94-09642-2	Sequence 2, Appli
43	182	15.8	329	2	US-08-456-104-2	Sequence 2, Appli
44	182	15.8	329	2	US-08-101-624-2	Sequence 2, Appli
45	182	15.8	329	3	US-08-479-744A-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-147-772-2

Sequence 2, Application US/08147772

Patent No. 5858776

GENERAL INFORMATION:
 APPLICANT: Ostrand-Rosenberg, Suzanne
 APPLICANT: Baskar, Sivasubramanian
 APPLICANT: Glimcher, Laurie H.
 APPLICANT: Freeman, Gordon J.
 APPLICANT: Nadler, Lee M.
 TITLE OF INVENTION: Tumor Cells With Increased Immunogenicity
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
  ADDRESSEE: LAHIVE & COCKFIELD
  STREET: 60 State Street, Suite 510
  CITY: Boston
  STATE: Massachusetts
  COUNTRY: USA
  ZIP: 02109
 COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/147,772
  FILING DATE:
  CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
  APPLICATION NUMBER:
  FILING DATE:
 ATTORNEY/AGENT INFORMATION:
  NAME: Mandragouras, Amy E.
  REGISTRATION NUMBER: 36,207
  REFERENCE/DOCKET NUMBER: RPI-003
 TELECOMMUNICATION INFORMATION:
  TELEPHONE: (617) 227-7400
  TELEFAX: (617) 227-5941
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
  LENGTH: 288 amino acids
  TYPE: amino acid
  TOPOLOGY: linear
 MOLECULE TYPE: protein
  DESCRIPTION: B cell activation antigen; natural ligand
  DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein
 FEATURE:
  NAME/KEY: signal sequence
  LOCATION: -34 to -1
  IDENTIFICATION METHOD: amino terminal sequencing of

OTHER INFORMATION: soluble protein
IDENTIFICATION METHOD: hydrophobic

FEATURE:
NAME/KEY: extracellular domain
LOCATION: 1 to 208
IDENTIFICATION METHOD: similarity with known sequence

FEATURE:
NAME/KEY: transmembrane domain
LOCATION: 209 to 235
IDENTIFICATION METHOD: similarity with known sequence

FEATURE:
NAME/KEY: intracellular domain
LOCATION: 236 to 254
IDENTIFICATION METHOD: similarity with known sequence

FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 19 to 21
IDENTIFICATION METHOD: similarity with known sequence

FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 173 to 175
IDENTIFICATION METHOD: similarity with known sequence

FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 55 to 57
IDENTIFICATION METHOD: similarity with known sequence

FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 64 to 66
IDENTIFICATION METHOD: similarity with known sequence

FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 152 to 154
IDENTIFICATION METHOD: similarity with known sequence

FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 177 to 179
IDENTIFICATION METHOD: similarity with known sequence

FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 192 to 194
IDENTIFICATION METHOD: similarity with known sequence

FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 198 to 200
IDENTIFICATION METHOD: similarity with known sequence

FEATURE:
NAME/KEY: Ig V-set domain
LOCATION: 1 to 104
IDENTIFICATION METHOD: similarity with known sequence

FEATURE:
NAME/KEY: Ig C-set domain
LOCATION: 105 to 202
IDENTIFICATION METHOD: similarity with known sequence

Query Match   100.0%; Score 1149; DB 2; Length 288;
Best Local Similarity 100.0%; Pred. No. 5.2e-113;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86

Qy   61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPPTPS 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   87 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPPTPS 146

Qy  121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206

Qy  181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
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Db  207 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242
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RESULT 2
US-08-456-104-6
Sequence 6, Application US/08456104
Patent No. 5861310
GENERAL INFORMATION:
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
APPLICANT: Gray, Gary S.
TITLE OF INVENTION: TUMOR CELLS MODIFIED TO EXPRESS B7-2 AND B7-3 WITH INCREASE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,104
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/101,624;
FILING DATE: 26-JUL-1993;
APPLICATION NUMBER: 08/109,393;
APPLICATION NUMBER: 19-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:

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;  LENGTH:  288 amino acids
;  TYPE:  amino acid
;  TOPOLOGY:  linear
;  MOLECULE TYPE:  protein
US-08-456-104-6

Query Match    100.0%;  Score 1149;  DB 2;  Length 288;
Best Local Similarity   100.0%;  Pred. No. 5.2e-113;
Matches  216;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy      1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86

Qy     61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     87 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 146

Qy    121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206

Qy    181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
          ||||||||||||||||||||||||||||||||||||
Db    207 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242


RESULT   3
US-08-101-624-23
Sequence 23, Application US/08101624
Patent No. 5942607

;  GENERAL INFORMATION:
;  APPLICANT:  Freeman, Gordon J.
;  APPLICANT:  Nadler, Lee M.
;  APPLICANT:  Gray, Gary S.
;  TITLE OF INVENTION:  No. 5942607el CTLA4/CD28 Ligands and
;  TITLE OF INVENTION:  Uses Therefor
;  NUMBER OF SEQUENCES:  25
;  CORRESPONDENCE ADDRESS:
;    ADDRESSEE:  LAHIVE & COCKFIELD
;    STREET:  60 State Street, Suite 510
;    CITY:  Boston
;    STATE:  Massachusetts
;    COUNTRY:  USA
;    ZIP:  02109
;  COMPUTER READABLE FORM:
;    MEDIUM TYPE:  Floppy disk
;    COMPUTER:  IBM PC compatible
;    OPERATING SYSTEM:  PC-DOS/MS-DOS
;    SOFTWARE:  Patentin Release #1.0, Version #1.25
;  CURRENT APPLICATION DATA:
;    APPLICATION NUMBER:  US/08/101,624
;    FILING DATE:  26-JUL-1993
;    CLASSIFICATION:  514
;  PRIOR APPLICATION DATA:
;    APPLICATION NUMBER:
;  FILING DATE:
;  ATTORNEY/AGENT INFORMATION:
;    NAME:  Mandragouras, Amy E.
;    REGISTRATION NUMBER:  36,207
;  REFERENCE/DOCKET NUMBER:  RPI-004
;  TELECOMMUNICATION INFORMATION:
;    TELEPHONE:  (617) 227-7400
;    TELEFAX:  (617) 227-5941
;  INFORMATION FOR SEQ ID NO: 23:
;  SEQUENCE CHARACTERISTICS:
;    LENGTH:  288 amino acids
;    TYPE:  amino acid
;    TOPOLOGY:  linear
;  MOLECULE TYPE:  protein
;  DESCRIPTION:  B cell activation antigen; natural ligand
;  DESCRIPTION:  for CD28 T cell surface antigen; transmembrane protein
```

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;  FEATURE:
;    NAME/KEY:  signal sequence
;    LOCATION:  -34 to -1
;    IDENTIFICATION METHOD:  amino terminal sequencing of
;    OTHER INFORMATION:  hydrophobic
;  FEATURE:
;    NAME/KEY:  extracellular domain
;    LOCATION:  1 to 208
;    IDENTIFICATION METHOD:  soluble protein
;    IDENTIFICATION METHOD:  similarity with known
;                           sequence
;  FEATURE:
;    NAME/KEY:  transmembrane domain
;    LOCATION:  209 to 235
;    IDENTIFICATION METHOD:  similarity with known
;                           sequence
;  FEATURE:
;    NAME/KEY:  intracellular domain
;    LOCATION:  236 to 254
;    IDENTIFICATION METHOD:  similarity with known
;                           sequence
;  FEATURE:
;    NAME/KEY:  N-linked glycosylation
;    LOCATION:  19 to 21
;    IDENTIFICATION METHOD:  similarity with known
;                           sequence
;  FEATURE:
;    NAME/KEY:  N-linked glycosylation
;    LOCATION:  55 to 57
;    IDENTIFICATION METHOD:  similarity with known
;                           sequence
;  FEATURE:
;    NAME/KEY:  N-linked glycosylation
;    LOCATION:  64 to 66
;    IDENTIFICATION METHOD:  similarity with known
;                           sequence
;  FEATURE:
;    NAME/KEY:  N-linked glycosylation
;    LOCATION:  152 to 154
;    IDENTIFICATION METHOD:  similarity with known
;                           sequence
;  FEATURE:
;    NAME/KEY:  N-linked glycosylation
;    LOCATION:  173 to 175
;    IDENTIFICATION METHOD:  similarity with known
;                           sequence
;  FEATURE:
;    NAME/KEY:  N-linked glycosylation
;    LOCATION:  177 to 179
;    IDENTIFICATION METHOD:  similarity with known
;                           sequence
;  FEATURE:
;    NAME/KEY:  N-linked glycosylation
;    LOCATION:  192 to 194
;    IDENTIFICATION METHOD:  similarity with known
;                           sequence
;  FEATURE:
;    NAME/KEY:  N-linked glycosylation
;    LOCATION:  198 to 200
;    IDENTIFICATION METHOD:  similarity with known
;                           sequence
;  FEATURE:
;    NAME/KEY:  Ig V-set domain
;    LOCATION:  1 to 104
;    IDENTIFICATION METHOD:  similarity with known
;                           sequence
;  FEATURE:
;    NAME/KEY:  Ig C-set domain
;    LOCATION:  105 to 202
;    IDENTIFICATION METHOD:  similarity with known
;                           sequence
;  PUBLICATION INFORMATION:
;    AUTHORS:  FREEMAN, GORDON J.
```

```
;       AUTHORS:    FREEDMAN, ARNOLD S.
;       AUTHORS:    SEGIL, JEFFREY M.
;       AUTHORS:    LEE, GRACE
;       AUTHORS:    WHITMAN, JAMES F.
;       AUTHORS:    NADLER, LEE M.
;       TITLE:      B7, A New Member Of The Ig Superfamily With
;                   Unique Expression On Activated And Neoplastic B Cells
;       JOURNAL:    The Journal of Immunology
;       VOLUME:     143
;       ISSUE:      8
;       PAGES:      2714-2722
;       DATE:       15-OCT-1989
US-08-101-624-23    RELEVANT RESIDUES IN SEQ ID NO: 23: From -26 to 262

Query Match    100.0%;  Score 1149;  DB 2;  Length 288;
Best Local Similarity  100.0%;  Pred. No. 5.2e-113;
Matches 216;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
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Db   27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86

Qy   61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADPPTPS 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   87 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADPPTPS 146

Qy  121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
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Db  147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206

Qy  181 NMTTNHSFMCLIKYGHLRVNQTFNWNNTTKQEHFPDN 216
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Db  207 NMTTNHSFMCLIKYGHLRVNQTFNWNNTTKQEHFPDN 242
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RESULT 4
US-08-751-767A-6
;       Sequence 6, Application US/08751767A
;       Patent No. 5994104
;       GENERAL INFORMATION:
;          APPLICANT:  ANDERSON, ROBERT J.
;          APPLICANT:  GRANT, HUGH
;          APPLICANT:  MACDONALD, IAN D.
;          TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;          NUMBER OF SEQUENCES:  80
;          CORRESPONDENCE ADDRESS:
;             ADDRESSEE:  NIXON & VANDERHYE P.C.
;             STREET:  1100 NORTH GLEBE ROAD
;             CITY:  ARLINGTON
;             STATE:  VA
;             COUNTRY:  USA
;             ZIP:  22201
;          COMPUTER READABLE FORM:
;             MEDIUM TYPE:  Floppy disk
;             COMPUTER:  IBM PC compatible
;             OPERATING SYSTEM:  PC-DOS/MS-DOS
;             SOFTWARE:  PatentIn Release #1.0, Version #1.30
;          CURRENT APPLICATION DATA:
;             APPLICATION NUMBER:  US/08/751,767A
;             FILING DATE:  08-NOV-1996
;             CLASSIFICATION:  536
;          ATTORNEY/AGENT INFORMATION:
;             NAME:  SADOFF, B.J.
;             REGISTRATION NUMBER:  36,663
;             REFERENCE/DOCKET NUMBER:  117-221
;          TELECOMMUNICATION INFORMATION:
;             TELEPHONE:  703164100
;             TELEFAX:  703164091
;       INFORMATION FOR SEQ ID NO:  6:
;          SEQUENCE CHARACTERISTICS:
;             LENGTH:  288 amino acids
;             TYPE:  amino acid
;             TOPOLOGY:  linear
;             MOLECULE TYPE:  protein
US-08-751-767A-6

Query Match    100.0%;  Score 1149;  DB 2;  Length 288;
Best Local Similarity  100.0%;  Pred. No. 5.2e-113;
Matches 216;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86

Qy   61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADPPTPS 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   87 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADPPTPS 146

Qy  121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206

Qy  181 NMTTNHSFMCLIKYGHLRVNQTFNWNNTTKQEHFPDN 216
        |||||||||||||||||||||||||||||||||||||
Db  207 NMTTNHSFMCLIKYGHLRVNQTFNWNNTTKQEHFPDN 242
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RESULT 5
US-08-153-262-2
;       Sequence 2, Application US/08153262
;       Patent No. 6071716
;       GENERAL INFORMATION:
;          APPLICANT:  FREEMAN, GORDON J.
;          APPLICANT:  FREEMAN, ARNOLD S.
;          APPLICANT:  NADLER, LEE M.
;          TITLE OF INVENTION:  DNA Encoding B7, A New Member
;          TITLE OF INVENTION:  Of The IgG Superfamily With Unique Expression On
;          TITLE OF INVENTION:  Activated And Neoplastic B Cells.
;          NUMBER OF SEQUENCES:  4
;          CORRESPONDENCE ADDRESS:
;             ADDRESSEE:  The Dana-Farber Cancer Institute
;             STREET:  44 Binney Street
;             CITY:  Boston
;             STATE:  Massachusetts
;             COUNTRY:  U.S.A.
;             ZIP:  02115
;          COMPUTER READABLE FORM:
;             MEDIUM TYPE:  Diskette, 3.50 inch, 720kb storage
;             COMPUTER:  IBM Personal System 2; Model 30
;             OPERATING SYSTEM:  MS/DOS
;             SOFTWARE:  WordPerfect 5.0
;          CURRENT APPLICATION DATA:
;             APPLICATION NUMBER:  US/08/153,262
;             FILING DATE:
;             CLASSIFICATION:
;          PRIOR APPLICATION DATA:
;             APPLICATION NUMBER:  US 07/751,306
;             FILING DATE:  28-AUG-1991
;          ATTORNEY/AGENT INFORMATION:
;             NAME:  HART, JULIA D.
;             REGISTRATION NUMBER:  33132
;             REFERENCE/DOCKET NUMBER:  DFCI-116.1
;          TELECOMMUNICATION INFORMATION:
;             TELEPHONE:  (203) 259-2846
;             TELEFAX:  (203) 255-8900
;       INFORMATION FOR SEQ ID NO:  2:
;          SEQUENCE CHARACTERISTICS:
;             LENGTH:  288 amino acids
;             TYPE:  amino acid
;             TOPOLOGY:  linear
;          MOLECULE TYPE:  protein
;          DESCRIPTION:  B cell activation antigen; natural ligand
;          DESCRIPTION:  for CD28 T cell surface antigen; transmembrane protein
```

FEATURE:
  NAME/KEY: signal sequence
  LOCATION: -34 to -1
  IDENTIFICATION METHOD: amino terminal sequencing of
  OTHER INFORMATION: hydrophobic
FEATURE:
  NAME/KEY: extracellular domain
  LOCATION: 1 to 208
  IDENTIFICATION METHOD: soluble protein
FEATURE:
  NAME/KEY: transmembrane domain
  LOCATION: 209 to 235
  IDENTIFICATION METHOD: similarity with known
  IDENTIFICATION METHOD: sequence
FEATURE:
  NAME/KEY: intracellular domain
  LOCATION: 236 to 254
  IDENTIFICATION METHOD: similarity with known
  IDENTIFICATION METHOD: sequence
FEATURE:
  NAME/KEY: N-linked glycosylation
  LOCATION: 19 to 21
  IDENTIFICATION METHOD: similarity with known
  IDENTIFICATION METHOD: sequence
FEATURE:
  NAME/KEY: N-linked glycosylation
  LOCATION: 55 to 57
  IDENTIFICATION METHOD: similarity with known
  IDENTIFICATION METHOD: sequence
FEATURE:
  NAME/KEY: N-linked glycosylation
  LOCATION: 64 to 66
  IDENTIFICATION METHOD: similarity with known
  IDENTIFICATION METHOD: sequence
FEATURE:
  NAME/KEY: N-linked glycosylation
  LOCATION: 152 to 154
  IDENTIFICATION METHOD: similarity with known
  IDENTIFICATION METHOD: sequence
FEATURE:
  NAME/KEY: N-linked glycosylation
  LOCATION: 173 to 175
  IDENTIFICATION METHOD: similarity with known
  IDENTIFICATION METHOD: sequence
FEATURE:
  NAME/KEY: N-linked glycosylation
  LOCATION: 177 to 179
  IDENTIFICATION METHOD: similarity with known
  IDENTIFICATION METHOD: sequence
FEATURE:
  NAME/KEY: N-linked glycosylation
  LOCATION: 192 to 194
  IDENTIFICATION METHOD: similarity with known
  IDENTIFICATION METHOD: sequence
FEATURE:
  NAME/KEY: N-linked glycosylation
  LOCATION: 198 to 200
  IDENTIFICATION METHOD: similarity with known
  IDENTIFICATION METHOD: sequence
FEATURE:
  NAME/KEY: Ig V-set domain
  LOCATION: 1 to 104
  IDENTIFICATION METHOD: similarity with known
  IDENTIFICATION METHOD: sequence
FEATURE:
  NAME/KEY: Ig C-set domain
  LOCATION: 105 to 202
  IDENTIFICATION METHOD: similarity with known
  IDENTIFICATION METHOD: sequence
PUBLICATION INFORMATION:
  AUTHORS: FREEMAN, GORDON J.

  AUTHORS: FREEDMAN, ARNOLD S.
  AUTHORS: SEGIL, JEFFREY M.
  AUTHORS: LEE, GRACE
  AUTHORS: WHITMAN, JAMES F.
  AUTHORS: NADLER, LEE M.
  TITLE: B7, A New Member Of The Ig Superfamily With
  TITLE: Unique Expression On Activated And Neoplastic B Cells
  JOURNAL: The Journal of Immunology
  VOLUME: 143
  ISSUE: 8
  PAGES: 2714-2722
  DATE: 15-OCT-1989

US-08-153-262-2
  RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262

Query Match   100.0%; Score 1149; DB 3; Length 288;
Best Local Similarity   100.0%; Pred. No. 5.2e-113;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86

Qy   61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   87 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 146

Qy   121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206

Qy   181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
         |||||||||||||||||||||||||||||||||||
Db   207 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242

RESULT 6
US-08-479-744A-29
Sequence 29, Application US/08479744A
Patent No. 6084067
GENERAL INFORMATION:
  APPLICANT: Freeman, Gordon J.
  APPLICANT: Nadler, Lee M.
  APPLICANT: Gray, Gary S.
  TITLE OF INVENTION: No. 6084067el CTLA4/CD28 Ligands and
  TITLE OF INVENTION: Uses Therefor
  NUMBER OF SEQUENCES: 55
  CORRESPONDENCE ADDRESS:
  ADDRESSEE: LAHIVE & COCKFIELD, LLP
  STREET: 60 State Street
  CITY: Boston
  STATE: Massachusetts
  COUNTRY: USA
  ZIP: 02109
  COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: Patentin Release #1.0, Version #1.25
  CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/479,744A
  FILING DATE: June 7, 1995
  PRIOR APPLICATION DATA:
  CLASSIFICATION: 435
  APPLICATION NUMBER: 08/280,757
  FILING DATE: 26-JUL-1994
  APPLICATION NUMBER: 08/109,393
  FILING DATE: 28-AUG-1993
  APPLICATION NUMBER: 08/101,624
  FILING DATE: 26-JULY-1993
  APPLICATION NUMBER: 08/147,773
  FILING DATE: 3-NOV-1993

ATTORNEY/AGENT INFORMATION:
　NAME: Mandragouras, Amy E.
　REGISTRATION NUMBER: 36,207
　REFERENCE/DOCKET NUMBER: RPI-004CP3
TELECOMMUNICATION INFORMATION:
　TELEPHONE: (617) 227-7400
　TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 29:
　SEQUENCE CHARACTERISTICS:
　　LENGTH: 288 amino acids
　　TYPE: amino acid
　　TOPOLOGY: linear
　MOLECULE TYPE: protein
　DESCRIPTION: B cell activation antigen; natural ligand
　DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein
　FEATURE:
　　NAME/KEY: signal sequence
　　LOCATION: -34 to -1
　　IDENTIFICATION METHOD: amino terminal sequencing of
　　IDENTIFICATION METHOD: soluble protein
　　OTHER INFORMATION: hydrophobic
　FEATURE:
　　NAME/KEY: extracellular domain
　　LOCATION: 1 to 208
　　IDENTIFICATION METHOD: similarity with known
　　IDENTIFICATION METHOD: sequence
　FEATURE:
　　NAME/KEY: transmembrane domain
　　LOCATION: 209 to 235
　　IDENTIFICATION METHOD: similarity with known
　　IDENTIFICATION METHOD: sequence
　FEATURE:
　　NAME/KEY: intracellular domain
　　LOCATION: 236 to 254
　　IDENTIFICATION METHOD: similarity with known
　　IDENTIFICATION METHOD: sequence
　FEATURE:
　　NAME/KEY: N-linked glycosylation
　　LOCATION: 19 to 21
　　IDENTIFICATION METHOD: similarity with known
　　IDENTIFICATION METHOD: sequence
　FEATURE:
　　NAME/KEY: N-linked glycosylation
　　LOCATION: 55 to 57
　　IDENTIFICATION METHOD: similarity with known
　　IDENTIFICATION METHOD: sequence
　FEATURE:
　　NAME/KEY: N-linked glycosylation
　　LOCATION: 64 to 66
　　IDENTIFICATION METHOD: similarity with known
　　IDENTIFICATION METHOD: sequence
　FEATURE:
　　NAME/KEY: N-linked glycosylation
　　LOCATION: 152 to 154
　　IDENTIFICATION METHOD: similarity with known
　　IDENTIFICATION METHOD: sequence
　FEATURE:
　　NAME/KEY: N-linked glycosylation
　　LOCATION: 173 to 175
　　IDENTIFICATION METHOD: similarity with known
　　IDENTIFICATION METHOD: sequence
　FEATURE:
　　NAME/KEY: N-linked glycosylation
　　LOCATION: 177 to 179
　　IDENTIFICATION METHOD: similarity with known
　　IDENTIFICATION METHOD: sequence
　FEATURE:
　　NAME/KEY: N-linked glycosylation
　　LOCATION: 192 to 194
　　IDENTIFICATION METHOD: similarity with known
　　IDENTIFICATION METHOD: sequence
　FEATURE:
　　NAME/KEY: N-linked glycosylation
　　LOCATION: 198 to 200
　　IDENTIFICATION METHOD: similarity with known
　　IDENTIFICATION METHOD: sequence
　FEATURE:
　　NAME/KEY: Ig V-set domain
　　LOCATION: 1 to 104
　　IDENTIFICATION METHOD: similarity with known
　　IDENTIFICATION METHOD: sequence
　FEATURE:
　　NAME/KEY: Ig C-set domain
　　LOCATION: 105 to 202
　　IDENTIFICATION METHOD: similarity with known
　　IDENTIFICATION METHOD: sequence
　PUBLICATION INFORMATION:
　　AUTHORS: FREEMAN, GORDON J.
　　AUTHORS: FREEDMAN, ARNOLD S.
　　AUTHORS: SEGIL, JEFFREY M.
　　AUTHORS: LEE, GRACE
　　AUTHORS: WHITMAN, JAMES F.
　　AUTHORS: NADLER, LEE M.
　　TITLE: B7, A New Member Of The Ig Superfamily With
　　TITLE: Unique Expression On Activated And Neoplastic B Cells
　　JOURNAL: The Journal of Immunology
　　VOLUME: 143
　　ISSUE: 8
　　PAGES: 2714-2722
　　DATE: 15-OCT-1989
　RELEVANT RESIDUES IN SEQ ID NO: 29: From -26 to 262
US-08-479-744A-29

Query Match　　　　100.0%;　Score 1149;　DB 3;　Length 288;
Best Local Similarity　100.0%;　Pred. No. 5.2e-113;
Matches　216;　Conservative　0;　Mismatches　0;　Indels　0;　Gaps　0;

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Qy    1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86

Qy   61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   87 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 146

Qy  121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206

Qy  181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
          ||||||||||||||||||||||||||||||||||||
Db  207 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242
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RESULT 7
US-08-280-757B-29
Sequence 29, Application US/08280757B
Patent No. 6130316
GENERAL INFORMATION:
　APPLICANT: Freeman, Gordon J.
　APPLICANT: Nadler, Lee M.
　APPLICANT: Gray, Gary S.
　APPLICANT: Greenfield, Edward
　TITLE OF INVENTION: No. 6130316e1 CTLA4/CD28 Ligands and
　TITLE OF INVENTION: Uses Therefor
　NUMBER OF SEQUENCES: 53
　CORRESPONDENCE ADDRESS:
　　ADDRESSEE: LAHIVE & COCKFIELD
　　STREET: 60 State Street, Suite 510
　　CITY: Boston
　　STATE: Massachusetts
　　COUNTRY: USA
　　ZIP: 02109
　COMPUTER READABLE FORM:
　　MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/280,757B
FILING DATE: 26-JUL-1994
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/101,624
FILING DATE: 26-JULY-1993
APPLICATION NUMBER: 08/109,393
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: 08/147,773
FILING DATE: 3-NOV-1993

ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-004CP2

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 29:

SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
DESCRIPTION: B cell activation antigen; natural ligand
for CD28 T cell surface antigen; transmembrane protein

FEATURE:
NAME/KEY: signal sequence
LOCATION: -34 to -1
IDENTIFICATION METHOD: amino terminal sequencing of
IDENTIFICATION METHOD: soluble protein
OTHER INFORMATION: hydrophobic

FEATURE:
NAME/KEY: extracellular domain
LOCATION: 1 to 208
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence

FEATURE:
NAME/KEY: transmembrane domain
LOCATION: 209 to 235
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence

FEATURE:
NAME/KEY: intracellular domain
LOCATION: 236 to 254
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence

FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 19 to 21
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence

FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 55 to 57
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence

FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 64 to 66
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence

FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 152 to 154
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence

FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 173 to 175

IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence

FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 177 to 179
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence

FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 192 to 194
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence

FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 198 to 200
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence

FEATURE:
NAME/KEY: Ig V-set domain
LOCATION: 1 to 104
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence

FEATURE:
NAME/KEY: Ig C-set domain
LOCATION: 105 to 202
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence

US-08-280-757B-29

Query Match   100.0%; Score 1149; DB 4;   Length 288;
Best Local Similarity   100.0%; Pred. No. 5.2e-113;
Matches   216; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
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Db   27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86

Qy   61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   87 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 146

Qy 121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206

Qy 181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
         ||||||||||||||||||||||||||||||||||||
Db 207 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242

RESULT   8
US-09-159-135-2

Sequence 2, Application US/09159135

Patent No. 6149905

GENERAL INFORMATION:
APPLICANT: Ostrand-Rosenberg, Suzanne
APPLICANT: Baskar, Sivasubramanian

APPLICANT: Glimcher, Laurie H.
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
TITLE OF INVENTION: Tumor Cells With Increased Immunogenicity
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/159,135
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/147,772
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: B cell activation antigen; natural ligand
for CD28 T cell surface antigen; transmembrane protein
FEATURE:
NAME/KEY: signal sequence
LOCATION: -34 to -1
IDENTIFICATION METHOD: amino terminal sequencing of
IDENTIFICATION METHOD: soluble protein
OTHER INFORMATION: hydrophobic
FEATURE:
NAME/KEY: extracellular domain
LOCATION: 1 to 208
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: transmembrane domain
LOCATION: 209 to 235
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: intracellular domain
LOCATION: 236 to 254
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 19 to 21
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 55 to 57
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 64 to 66

IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 152 to 154
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 173 to 175
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 192 to 194
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 177 to 179
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 198 to 200
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig V-set domain
LOCATION: 1 to 104
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig C-set domain
LOCATION: 105 to 202
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence

PUBLICATION INFORMATION:
AUTHORS: FREEMAN, GORDON J.
AUTHORS: FREEMAN, ARNOLD S.
AUTHORS: SEGIL, JEFFREY M.
AUTHORS: LEE, GRACE
AUTHORS: WHITMAN, JAMES F.
AUTHORS: NADLER, LEE M.
TITLE: B7, A New Member Of The Ig Superfamily With
TITLE: Unique Expression On Activated And Neoplastic B Cells
JOURNAL: The Journal of Immunology
VOLUME: 143
ISSUE: 8
PAGES: 2714-2722
DATE: 15-OCT-1989
RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262

US-09-159-135-2

Query Match   100.0%;   Score 1149;   DB 4;   Length 288;
Best Local Similarity 100.0%;   Pred. No. 5.2e-113;
Matches 216;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

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Qy      1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86

Qy     61 YKNRIFLPDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     87 YKNRIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 146

Qy    121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206

Qy    181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
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Db   207 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242

RESULT 9
US-08-205-697A-19
Sequence 19, Application US/08205697A
Patent No. 6218510
GENERAL INFORMATION:
  APPLICANT: Sharpe, Arlene H.
  APPLICANT: Borriello, Francescopaulo
  APPLICANT: Freeman, Gordon J.
  APPLICANT: Nadler, Lee M.
  TITLE OF INVENTION: No. 6218510el Forms of T Cell Costimulatory Molecules
  TITLE OF INVENTION: and Uses Therefor
  NUMBER OF SEQUENCES: 61
  CORRESPONDENCE ADDRESS:
  ADDRESSEE: LAHIVE & COCKFIELD
  STREET: 60 State Street, suite 510
  CITY: Boston
  STATE: Massachusetts
  COUNTRY: USA
  ZIP: 02109-1875
  COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: ASCII Text
  CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/205,697A
  FILING DATE: 02-Mar-1994
  ATTORNEY/AGENT INFORMATION:
  NAME: Mandragouras, Amy E.
  REGISTRATION NUMBER: 36,207
  REFERENCE/DOCKET NUMBER: BWI-120
  TELECOMMUNICATION INFORMATION:
  TELEPHONE: (617)227-7400
  TELEFAX: (617)227-5941
  INFORMATION FOR SEQ ID NO: 19:
  SEQUENCE CHARACTERISTICS:
  LENGTH: 288 amino acids
  TYPE: amino acid
  TOPOLOGY: linear
  MOLECULE TYPE: protein
US-08-205-697A-19

Query Match          100.0%;   Score 1149;  DB 4;   Length 288;
Best Local Similarity 100.0%;  Pred. No. 5.2e-113;
Matches 216; Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy   1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
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Db  27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86

Qy  61 YKNRTIFDITNNLSIVILALRPSDEGTYECVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  87 YKNRTIFDITNNLSIVILALRPSDEGTYECVLKYEKDAFKREHLAEVTLSVKADFPTPS 146

Qy 121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
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Db 147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206

Qy 181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
        ||||||||||||||||||||||||||||||||||||
Db 207 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242

RESULT 10
US-08-702-525-19
Sequence 19, Application US/08702525
Patent No. 6294660
GENERAL INFORMATION:
  APPLICANT: Sharpe, Sharpe
```

```
  APPLICANT: Borriello, Francescopaolo
  APPLICANT: Freeman, Gordon
  APPLICANT: Nadler, Lee
  TITLE OF INVENTION: No. 6294660el Forms of T Cell Costimulatory
  TITLE OF INVENTION: Molecules and Uses Therefor
  NUMBER OF SEQUENCES: 65
  CORRESPONDENCE ADDRESS:
  ADDRESSEE: LAHIVE & COCKFIELD
  STREET: 28 State Street
  CITY: Boston
  STATE: Massachusetts
  COUNTRY: USA
  ZIP: 02109-1875
  COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: ASCII Text
  CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/702,525
  FILING DATE:
  PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 08/205,697
  FILING DATE: 02-Mar-1994
  ATTORNEY/AGENT INFORMATION:
  NAME: Mandragouras, Amy E.
  REGISTRATION NUMBER: 36,207
  REFERENCE/DOCKET NUMBER: BWI-120CPUS
  TELECOMMUNICATION INFORMATION:
  TELEPHONE: (617)227-7400
  TELEFAX: (617)227-5941
  INFORMATION FOR SEQ ID NO: 19:
  SEQUENCE CHARACTERISTICS:
  LENGTH: 288 amino acid
  TYPE: amino acid
  TOPOLOGY: linear
  MOLECULE TYPE: protein
US-08-702-525-19

Query Match          100.0%;   Score 1149;  DB 4;   Length 288;
Best Local Similarity 100.0%;  Pred. No. 5.2e-113;
Matches 216; Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy   1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86

Qy  61 YKNRTIFDITNNLSIVILALRPSDEGTYECVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  87 YKNRTIFDITNNLSIVILALRPSDEGTYECVLKYEKDAFKREHLAEVTLSVKADFPTPS 146

Qy 121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206

Qy 181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
        ||||||||||||||||||||||||||||||||||||
Db 207 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242

RESULT 11
US-09-450-798-2
Sequence 2, Application US/09450798
Patent No. 6319709
GENERAL INFORMATION:
  APPLICANT: Ostrand-Rosenberg, Suzanne
  APPLICANT: Baskar, Sivasubramanian
  APPLICANT: Glincher, Laurie H.
  APPLICANT: Freeman, Gordon J.
  APPLICANT: Nadler, Lee M.
  TITLE OF INVENTION: Tumor Cells With Increased Immunogenicity
  NUMBER OF SEQUENCES: 4
```

CORRESPONDENCE ADDRESS:
 ADDRESSEE: LAHIVE & COCKFIELD
 STREET: 60 State Street, Suite 510
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02109
COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/450,798
 FILING DATE: 29-NOV-1999
PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/147,772
 FILING DATE: 03-NOV-1993
ATTORNEY/AGENT INFORMATION:
 NAME: Mandragouras, Amy E.
 REGISTRATION NUMBER: 36,207
 REFERENCE/DOCKET NUMBER: RPI-003
TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400
 TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 288 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 DESCRIPTION: B cell activation antigen; natural ligand
 for CD28 T cell surface antigen; transmembrane protein
 OTHER INFORMATION: hydrophobic
 FEATURE:
 NAME/KEY: signal sequence
 LOCATION: -34 to -1
 IDENTIFICATION METHOD: amino terminal sequencing of
 IDENTIFICATION METHOD: soluble protein
 IDENTIFICATION METHOD: sequence
 FEATURE:
 NAME/KEY: extracellular domain
 LOCATION: 1 to 208
 IDENTIFICATION METHOD: similarity with known
 IDENTIFICATION METHOD: sequence
 FEATURE:
 NAME/KEY: transmembrane domain
 LOCATION: 209 to 235
 IDENTIFICATION METHOD: similarity with known
 IDENTIFICATION METHOD: sequence
 FEATURE:
 NAME/KEY: intracellular domain
 LOCATION: 236 to 254
 IDENTIFICATION METHOD: similarity with known
 IDENTIFICATION METHOD: sequence
 FEATURE:
 NAME/KEY: N-linked glycosylation
 LOCATION: 19 to 21
 IDENTIFICATION METHOD: similarity with known
 IDENTIFICATION METHOD: sequence
 FEATURE:
 NAME/KEY: N-linked glycosylation
 LOCATION: 55 to 57
 IDENTIFICATION METHOD: similarity with known
 IDENTIFICATION METHOD: sequence
 FEATURE:
 NAME/KEY: N-linked glycosylation
 LOCATION: 64 to 66
 IDENTIFICATION METHOD: similarity with known
 IDENTIFICATION METHOD: sequence
 FEATURE:
 NAME/KEY: N-linked glycosylation
 LOCATION: 152 to 154
 IDENTIFICATION METHOD: similarity with known

 IDENTIFICATION METHOD: sequence
 FEATURE:
 NAME/KEY: N-linked glycosylation
 LOCATION: 173 to 175
 IDENTIFICATION METHOD: similarity with known
 IDENTIFICATION METHOD: sequence
 FEATURE:
 NAME/KEY: N-linked glycosylation
 LOCATION: 177 to 179
 IDENTIFICATION METHOD: similarity with known
 IDENTIFICATION METHOD: sequence
 FEATURE:
 NAME/KEY: N-linked glycosylation
 LOCATION: 192 to 194
 IDENTIFICATION METHOD: similarity with known
 IDENTIFICATION METHOD: sequence
 FEATURE:
 NAME/KEY: N-linked glycosylation
 LOCATION: 198 to 200
 IDENTIFICATION METHOD: similarity with known
 IDENTIFICATION METHOD: sequence
 FEATURE:
 NAME/KEY: Ig V-set domain
 LOCATION: 1 to 104
 IDENTIFICATION METHOD: similarity with known
 IDENTIFICATION METHOD: sequence
 FEATURE:
 NAME/KEY: Ig C-set domain
 LOCATION: 105 to 202
 IDENTIFICATION METHOD: similarity with known
 IDENTIFICATION METHOD: sequence
 PUBLICATION INFORMATION:
 AUTHORS: FREEMAN, GORDON J.
 AUTHORS: FREEDMAN, ARNOLD S.
 AUTHORS: SEGIL, JEFFREY M.
 AUTHORS: WHITMAN, JAMES F.
 AUTHORS: NADLER, LEE M.
 AUTHORS: LEE, GRACE
 TITLE: B7, A New Member Of The Ig Superfamily With
 TITLE: Unique Expression On Activated And Neoplastic B Cells
 JOURNAL: The Journal of Immunology
 VOLUME: 143
 ISSUE: 8
 PAGES: 2714-2722
 DATE: 15-OCT-1989
 RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262

US-09-450-798-2

Query Match 100.0%; Score 1149; DB 4; Length 288;
Best Local Similarity 100.0%; Pred. No. 5.2e-113;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86

Qy 61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADPPTPS 120
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 87 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADPPTPS 146

Qy 121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206

Qy 181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
        ||||||||||||||||||||||||||||||||||||
Db 207 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242

RESULT 12
US-08-403-253A-2
; Sequence 2, Application US/0840325A

Patent No. 6352694

GENERAL INFORMATION:

; APPLICANT: June, Carl H.; Thompson, Craig B.; Nabel, Gary J.
; APPLICANT: Gray, Gary S.; Rennert, Paul D.
; TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,253A
; FILING DATE: March 10, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/253,964
; FILING DATE: 3 JUNE 1994
; APPLICATION NUMBER: US 08/073,223
; FILING DATE: 4 JUNE 1993
; APPLICATION NUMBER: US 08/200,947
; FILING DATE: 23 FEB 1994
; APPLICATION NUMBER: US 07/864,805
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 08/247,505
; FILING DATE: 23 MAY 1994
; APPLICATION NUMBER: US 07/864,866
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 08/218,155
; FILING DATE: 25 MAR 1994
; APPLICATION NUMBER: US 07/864,807
; FILING DATE: 7 APR 1992
; APPLICATION NUMBER: US 07/902,467
; FILING DATE: 16 JUNE 1992
; APPLICATION NUMBER: US 07/275,433
; FILING DATE: 23 NOV 1988
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-002CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214

INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 288 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: B cell activation antigen; natural ligand
; for CD28 T cell surface antigen; transmembrane protein
; FEATURE:
; NAME/KEY: signal sequence
; LOCATION: -34 to -1
; IDENTIFICATION METHOD: amino terminal sequencing of
; OTHER INFORMATION: hydrophobic
; soluble protein
; FEATURE:
; NAME/KEY: extracellular domain
; LOCATION: 1 to 208
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: transmembrane domain
; LOCATION: 209 to 235
; IDENTIFICATION METHOD: similarity with known

; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: intracellular domain
; LOCATION: 236 to 254
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: N-linked glycosylation
; LOCATION: 64 to 66
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: N-linked glycosylation
; LOCATION: 55 to 57
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: N-linked glycosylation
; LOCATION: 19 to 21
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: N-linked glycosylation
; LOCATION: 152 to 154
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: N-linked glycosylation
; LOCATION: 173 to 175
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: N-linked glycosylation
; LOCATION: 177 to 179
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: N-linked glycosylation
; LOCATION: 198 to 200
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: Ig V-set domain
; LOCATION: 192 to 194
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: Ig V-set domain
; LOCATION: 1 to 104
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: Ig C-set domain
; LOCATION: 105 to 202
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; PUBLICATION INFORMATION:
; AUTHORS: FREEMAN, GORDON J.
; AUTHORS: FREEDMAN, ARNOLD S.
; AUTHORS: SEGIL, JEFFREY M.
; AUTHORS: LEE, GRACE
; AUTHORS: WHITMAN, JAMES F.
; AUTHORS: NADLER, LEE M.
; TITLE: B7, A New Member Of The Ig Superfamily With
; Unique Expression On Activated And Neoplastic B Cells
; JOURNAL: The Journal of Immunology
; VOLUME: 143
; ISSUE: 8
; PAGES: 2714-2722
; DATE: 15-OCT-1989
; RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262

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Query Match                   100.0%;  Score 1149;  DB 4;   Length 288;
Best Local Similarity         100.0%;  Pred. No. 5.2e-113;
Matches 216;     Conservative    0;   Mismatches    0;   Indels    0;   Gaps    0;

Qy        1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
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Db       27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86

Qy       61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       87 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 146

Qy      121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELIYAVSSKLDF 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELIYAVSSKLDF 206

Qy      181 NMTTNHSFMCLIKYGHLRVNQTFNWNNTKQEHFPDN 216
            ||||||||||||||||||||||||||||||||||||
Db      207 NMTTNHSFMCLIKYGHLRVNQTFNWNNTKQEHFPDN 242

RESULT 13
PCT-US95-02576-19
; Sequence 19, Application PC/TUS9502576
; GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  Novel Forms of T Cell Costimulatory Molecules
;    TITLE OF INVENTION:  and Uses Therefor
;    NUMBER OF SEQUENCES:  65
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  60 State Street, Suite 510
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109-1875
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII Text
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/02576
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/205,697
;      FILING DATE:  02-Mar-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mandragouras, Amy E.
;      REGISTRATION NUMBER:  36,207
;      REFERENCE/DOCKET NUMBER:  BWI-120CPPC
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)227-7400
;      TELEFAX:  (617)227-5941
;      TELEX:  (617)227-5941
; INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  288 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US95-02576-19

Qy       61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
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Db       87 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 146

Qy      121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELIYAVSSKLDF 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELIYAVSSKLDF 206

Qy      181 NMTTNHSFMCLIKYGHLRVNQTFNWNNTKQEHFPDN 216
            ||||||||||||||||||||||||||||||||||||
Db      207 NMTTNHSFMCLIKYGHLRVNQTFNWNNTKQEHFPDN 242

RESULT 14
US-09-171-945-131
; Sequence 131, Application US/09171945
; Patent No. 6277599
; GENERAL INFORMATION:
;    APPLICANT:  Emery, Stephen
;    APPLICANT:  Copley, Clive Graham
;    APPLICANT:  Edge, Michael Derek
;    TITLE OF INVENTION:  Monoclonal Antibody to CEA, Conjugates Comprising Said
;    TITLE OF INVENTION:  Monoclonal Antibody, and Their Therapeutic Use in an Adept System
;    FILE REFERENCE:
;    CURRENT APPLICATION NUMBER:  US/09,171,945
;    CURRENT FILING DATE:  1998-10-29
;    PRIOR APPLICATION NUMBER:  GB9703103.3
;    PRIOR FILING DATE:  1997-02-14
;    PRIOR APPLICATION NUMBER:  GB9609405.7
;    PRIOR FILING DATE:  1996-05-04
;    PRIOR APPLICATION NUMBER:  PCT/GB97/01165
;    PRIOR FILING DATE:  1997-04-29
;    NUMBER OF SEQ ID NOS:  131
;    SEQ ID NO 131
;      LENGTH:  473
;      TYPE:  PRT
;      ORGANISM:  Artificial Sequence
;    FEATURE:
;      OTHER INFORMATION:  Description of Artificial Sequence: humanized
US-09-171-945-131

Query Match                   100.0%;  Score 1149;  DB 4;   Length 473;
Best Local Similarity         100.0%;  Pred. No. 1.1e-112;
Matches 216;     Conservative    0;   Mismatches    0;   Indels    0;   Gaps    0;

Qy        1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86

Qy       61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       87 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 146

Qy      121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELIYAVSSKLDF 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELIYAVSSKLDF 206

Qy      181 NMTTNHSFMCLIKYGHLRVNQTFNWNNTKQEHFPDN 216
            ||||||||||||||||||||||||||||||||||||
Db      207 NMTTNHSFMCLIKYGHLRVNQTFNWNNTKQEHFPDN 242

RESULT 15
US-09-460-384-36
; Sequence 36, Application US/09460384
; Patent No. 6337316
; GENERAL INFORMATION:
;    APPLICANT:  EL TAYAR, Nabil
;    APPLICANT:  BLECHNER, Steven
;    APPLICANT:  JAMESON, Brad
;    APPLICANT:  TEPPER, Mark
;    TITLE OF INVENTION:  CD28/CTLA-4 INHIBITING PEPTIDOMIMETICS,
```

PHARMACEUTICAL COMPOSITIONS THEREOF, AND METHOD OF USING

```
                   NUMBER OF SEQUENCES: 37
~                  CORRESPONDENCE ADDRESS:
~                     ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
~                     STREET: 624 Ninth Street N.W., Ste. 300
~                     CITY: Washington
~                     STATE: D.C.
~                     COUNTRY: U.S.A.
~                     ZIP: 20001
                   COMPUTER READABLE FORM:
                      MEDIUM TYPE: Floppy disk
                      COMPUTER: IBM PC compatible
                      OPERATING SYSTEM: PC-DOS/MS-DOS
                      SOFTWARE: Patentin Release #1.0, Version #1.30
                   CURRENT APPLICATION DATA:
                      APPLICATION NUMBER: US/09/460,384
                      FILING DATE: 13-Dec-1999
                      CLASSIFICATION: <Unknown>
                   PRIOR APPLICATION DATA:
                      APPLICATION NUMBER: PCT/US98/12312
                      FILING DATE: 11-JUN-1998
                      APPLICATION NUMBER: US 60/049,470
                      FILING DATE: 12-JUN-1997
                   ATTORNEY/AGENT INFORMATION:
                      NAME: YUN, Allen C
                      REGISTRATION NUMBER: 37,971
                      REFERENCE/DOCKET NUMBER: EL TAYAR-1A
                   TELECOMMUNICATION INFORMATION:
                      TELEPHONE: (202) 628-5197
                      TELEFAX: (202) 737-3528
~                  INFORMATION FOR SEQ ID NO: 36:
~                     SEQUENCE CHARACTERISTICS:
~                        LENGTH: 208 amino acids
~                        TYPE: amino acid
~                        STRANDEDNESS: single
~                        TOPOLOGY: linear
~                     MOLECULE TYPE: peptide
~                     SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-09-460-384-36
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Query Match      95.9%;   Score 1102;   DB 4;   Length 208;
Best Local Similarity   100.0%;   Pred. No. 2.8e-108;
Matches  208;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy    9 VIHVTKEVEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEYKNRTIFD 68
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Db    1 VIHVTKEVEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEYKNRTIFD 60

Qy   69 ITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPPTPSISDEIPT 128
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 ITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPPTPSISDEIPT 120

Qy  129 SNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFNMTTNHSF 188
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 SNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFNMTTNHSF 180

Qy  189 MCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
         ||||||||||||||||||||||||||||
Db  181 MCLIKYGHLRVNQTFNWNTTKQEHFPDN 208
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